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SARS VIRUS NUCLEOTIDE AND AMINO ACID SEQUENCES AND USES THEREOF

Abstract:

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The invention provides, in part, the genomic sequence of a putative coronavirus, the SARS virus, and provides novel nucleic acid and amino acid sequences that may be used, for example, for the diagnosis, prophylaxis, or therapy of a variety of SARS virus related disorders. Data supplied from the esp@cenet database - Worldwide c40

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(54) Title: SARS VIRUS NUCLEOTIDE AND AMINO ACID SEQUENCES AND USES THEREOF

(57) Abstract: The invention provides, in part, the genomic sequence of a putative coronavirus, the SARS virus, and provides novel nucleic acid and amino acid sequences that may be used, for example, for the diagnosis, prophylaxis, or therapy of a variety of SARS virus related disorders.



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SARS VIRUS NUCLEOTIDE AND AMINO ACID
SEQUENCES AND USES THEREOF

Field of the Invention

The invention is in the field of virology. More specifically, the invention is in the field of coronaviruses.

Background of the Invention

Severe acute respiratory syndrome (SARS), a worldwide outbreak of atypical pneumonia with an overall mortality rate of about 3 to 6%, has been attributed to a coronavirus following tests of causation according to Koch's postulates, including monkey inoculation (R. Munch, *Microbes Infect* 5, 69-74, Jan. 2003). The coronaviruses are members of a family of enveloped viruses that replicate in the cytoplasm of animal host cells (B. N. Fields et al., *Fields virology*, Lippincott Williams & Wilkins, Philadelphia, 4th ed., 2001). They are distinguished by the presence of a single-stranded plus sense RNA genome, approximately 30 kb in length, that has a 5' cap structure and 3' polyA tract. Hence the genome is essentially a very large mRNA. Upon infection of an appropriate host cell, the 5'-most open reading frame (ORF) of the viral genome is translated into a large polyprotein that is cleaved by viral-encoded proteases to release several nonstructural proteins including an RNA-dependent RNA polymerase (Pol) and an ATPase helicase (Hel). These proteins in turn are responsible for replicating the viral genome as well as generating nested transcripts that are used in the synthesis of the viral proteins. The mechanism by which these subgenomic mRNAs are made is not fully understood, however transcription regulating sequences (TRSs) at the 5' end of each gene may represent signals that regulate the discontinuous transcription of subgenomic mRNAs (sgmRNAs). The TRSs include a partially conserved core sequence (CS) that in some coronaviruses is 5'-CUAAAC-3'. Two major models have been proposed to explain the discontinuous transcription in coronaviruses and arterioviruses (M.M.C.Lai, D. Cavanagh, *Adv Virus Res.* 48,1(1997); S. G. Sawicki, D.L. Sawicki, *Adv.Exp. Med Biol.* 440,215(1998)). The

discovery of transcriptionally active, subgenomic-size minus strands containing the antileader sequence and transcription intermediates active in the synthesis of mRNAs (D. L. Sawicki et al., J. Gen Virol 82,386 (2001); S. G. Sawicki, D.L. Sawicki, J. Virol. 64,1050 (1990); M. Schaad, R.S.J. Baric, J. Virol. 68,8169(1994); P. B. Sethna et al.,
5 Proc. Natl. Acad. Sci. U.S.A. 86,5626 (1989)) favors the model of discontinuous transcription during the minus strand synthesis(S. G. Sawicki, D.L. Sawicki, Adv.Exp. Med Biol.440,215(1998)).

The coronaviral membrane proteins, including the major proteins S (Spike) and M (Membrane), are inserted into the endoplasmic reticulum Golgi intermediate
10 compartment (ERGIC) while full length replicated RNA (+ strands) assemble with the N (nucleocapsid) protein. This RNA-protein complex then associates with the M protein embedded in the membranes of the ER and virus particles form as the nucleocapsid complex buds into the ER. The virus then migrates through the Golgi complex and eventually exits the cell, likely by exocytosis (B. N. Fields et al., *Fields*
15 *virology*, Lippincott Williams & Wilkins, Philadelphia, 4th ed., 2001). The site of viral attachment to the host cell resides within the S protein.

The coronaviruses include a large number of viruses that infect different animal species. The predominant diseases associated with these viruses are respiratory and enteric infections, although hepatic and neurological diseases also occur with some
20 viruses. Coronaviruses are divided into three serotypes, Types I, II and III. Phylogenetic analysis of coronavirus sequences also identifies three main classes of these viruses, corresponding to each of the three serotypes. Type II coronaviruses contain a hemagglutinin esterase (HE) gene homologous to that of Influenza C virus. It is presumed that the precursor of the Type II coronaviruses acquired HE as a result of a
25 recombination event within a doubly infected host cell.

In view of the rapid worldwide dissemination of SARS, which has the potential of creating a pandemic, along with its alarming morbidity and mortality rates, it would be useful to have a better understanding of this coronavirus agent at the molecular level to provide diagnostics, vaccines, and therapeutics, and to support public health control
30 measures.

Summary of the Invention

In general, the invention provides the genomic sequence of a novel coronavirus, the SARS virus, and provides novel nucleic acid molecules encoding novel proteins that may be used, for example, for the diagnosis or therapy of a variety of SARS virus-related disorders.

In one aspect, the invention provides a substantially pure SARS virus nucleic acid molecule or fragment thereof, for example, a genomic RNA or DNA, cDNA, synthetic DNA, or mRNA molecule. In some embodiments, the nucleic acid molecule includes a sequence substantially identical to any of the sequences of SEQ ID NOs: 1-13, 15-18, 20-30, 90-159, 208, 209. In some embodiments, the nucleic acid molecule includes a sequence from SEQ ID NO: 1, SEQ ID NO:2, or SEQ ID NO: 15 or a fragment of these sequences. In alternative embodiments, the nucleic acid molecule may include a sequence substantially identical to SEQ ID NO: 1, SEQ ID NO:2, or SEQ ID NO: 15, or a fragment thereof. In alternative embodiments, the nucleic acid molecule may include a s2m motif (for example, a s2m sequence substantially identical to any of the sequence of SEQ ID NOs: 16, 17, and 18), a leader sequence (for example, a sequence substantially identical to the sequence of SEQ ID NO: 3), or a transcriptional regulatory sequence (for example, a sequence substantially identical to any of the sequence of SEQ ID NOs: 4-13 and 20-30). In alternative embodiments, the nucleic acid molecule includes a sequence substantially identical to any of the sequences of nucleotides 265-13,398; 13,398-21,485; 21,492 – 25,259; 25,268 – 26,092; 25,689 – 26,153; 26,117 – 26,347; 26,398 – 27,063; 27,074 – 27,265; 27,273 – 27,641; 27,638 – 27,772; 27,779 – 27,898; 27,864 – 28,118; 28,120 – 29,388; 28,130 – 28,426; 28,583 – 28,795; and 29,590 – 29,621 of SEQ ID NO: 15. In alternative embodiments, the nucleic acid molecule may encode a polyprotein or a polypeptide. In alternative embodiments, the invention provides a nucleic acid molecule including a sequence complementary to a SARS virus nucleotide sequence.

In an alternative aspect, the invention provides a substantially pure SARS virus polypeptide or fragment thereof, for example, a polyprotein, glycoprotein (for example, a matrix glycoprotein that may include a sequence substantially identical to the sequence of SEQ ID NO: 34), a transmembrane protein (for example, a multitransmembrane protein, a type I transmembrane protein, or a type II

transmembrane protein), a RNA binding protein, or a viral envelope protein. In alternative embodiments, the invention provides a replicase 1a protein, replicase 1b protein, a spike glycoprotein, a small envelope protein, a matrix glycoprotein, or a nucleocapsid protein. In alternative embodiments, the invention provides a nucleic acid molecule encoding a SARS virus polypeptide. In alternative embodiments, the SARS virus polypeptide includes an identifiable signal sequence (for example, a signal sequence substantially identical to the sequence of SEQ ID NOs: 76 or 85), a transmembrane domain (for example, a transmembrane domain substantially identical to any of the sequences of SEQ ID NOs: 77-86), a transmembrane anchor, a transmembrane helix, an ATP-binding domain, a nuclear localization signal, a hydrophilic domain, (for example, a hydrophilic domain substantially identical to the sequence of SEQ ID NOs: 87), or a lysine-rich sequence (for example, a sequence substantially identical to the sequence of SEQ ID NO: 14). In alternative embodiments, the SARS virus polypeptide may include a sequence substantially identical to any of the sequences of SEQ ID NOs: 14, 33-36, 64-74, and 76-87.

In alternative embodiments, the invention provides a vector (for example, a gene therapy vector or a cloning vector) including a SARS virus nucleic acid molecule (for example, a molecule including a sequence substantially identical to any of the sequences of SEQ ID NOs: 1-13, 15-18, 20-30, 90-159, 208, 209), or a host cell (for example, a mammalian cell, a yeast, a bacterium, or a nematode cell) including the vector.

In alternative embodiments, the invention provides a nucleic acid molecule having substantial nucleotide sequence identity (for example, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% complementarity) to a sequence encoding a SARS virus polypeptide or fragment thereof, for example where the fragment includes at least six amino acids, and where the nucleic acid molecule hybridizes under high stringency conditions to at least a portion of a SARS virus nucleic acid molecule.

In alternative embodiments, the invention provides a nucleic acid molecule having substantial nucleotide sequence identity (for example, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% complementarity) to a SARS virus nucleotide sequence, for example where the nucleic acid molecule includes at least ten nucleotides, and where

the nucleic acid molecule hybridizes under high stringency conditions to at least a portion of a SARS virus nucleic acid molecule.

In alternative embodiments, the invention provides a nucleic acid molecule comprising a sequence that is antisense to a SARS virus nucleic acid molecule, or an antibody (for example, a neutralizing antibody) that specifically binds to a SARS virus polypeptide.

In alternative embodiments, the invention provides a method for detecting a SARS epitope, such as a virion or polypeptide in a sample, by contacting the sample with an antibody that specifically binds a SARS epitope, such as a virus polypeptide, and determining whether the antibody specifically binds to the polypeptide. In alternative embodiments, the invention provides a method for detecting a SARS virus genome, gene, or homolog or fragment thereof in a sample by contacting a SARS virus nucleic acid molecule, for example where the nucleic acid molecule includes at least ten nucleotides, with a preparation of genomic DNA from the sample, under hybridization conditions providing detection of DNA sequences having nucleotide sequence identity to a SARS virus nucleic acid molecule. In alternative embodiments, the invention provides a method of targeting a protein for secretion from a cell, by attaching a signal sequence from a SARS virus polypeptide to the protein, such that the protein is secreted from the cell.

In alternative aspects, the invention provides a method for eliciting an immune response in an animal, by identifying an animal infected with or at risk for infection with a SARS virus and administering a SARS virus polypeptide or fragment thereof or fragment thereof, or administering a SARS virus nucleic acid molecule encoding a SARS virus polypeptide or fragment thereof to the animal. In alternative embodiments, the administering results in the production of an antibody in the mammal, or results in the generation of cytotoxic or helper T-lymphocytes in the mammal.

In alternative embodiments, the invention provides a kit for detecting the presence of a SARS virus nucleic acid molecule or polypeptide in a sample, where the kit includes a SARS virus nucleic acid molecule, or an antibody that specifically binds a SARS virus polypeptide.

In alternative aspects the invention provides a method for treating or preventing a SARS virus infection by identifying an animal (e.g., a human) infected with or at risk

for infection with a SARS virus, and administering a SARS virus nucleic acid molecule or polypeptide, or administering a compound that inhibits pathogenicity or replication of a SARS virus, to the animal. In alternative embodiments, the invention provides the use of a SARS virus nucleic acid molecule or polypeptide for treating or preventing a SARS virus infection.

In alternative aspects the invention provides a method of identifying a compound for treating or preventing a SARS virus infection, by contacting sample including a SARS virus nucleic acid molecule or contacting a SARS virus polypeptide with the compound, where an increase or decrease in the expression or activity of the nucleic acid molecule or the polypeptide identifies a compound for treating or preventing a SARS virus infection.

In alternative aspects the invention provides a vaccine (e.g., a DNA vaccine) including a SARS virus nucleic acid molecule or polypeptide.

In alternative aspects the invention provides a microarray including a plurality of elements, wherein each element includes one or more distinct nucleic acid or amino acid sequences, and where the sequences are selected from a SARS virus nucleic acid molecule or polypeptide, or a antibody that specifically binds a SARS virus nucleic acid molecule or polypeptide.

In alternative aspects the invention provides a computer readable record (e.g., a database) including distinct SARS virus nucleic acid or amino acid sequences.

A "SARS virus" is a virus putatively belonging to the coronavirus family and identified as the causative agent for sudden acute respiratory syndrome (SARS). A SARS virus nucleic acid molecule may include a sequence substantially identical to the nucleotide sequences described herein or fragments thereof. A SARS virus polypeptide may include a sequence substantially identical to a sequence encoded by a SARS virus nucleic acid molecule, or may include a sequence substantially identical to the polypeptide sequences described herein, or fragments thereof.

A compound is "substantially pure" when it is separated from the components that naturally accompany it. Typically, a compound is substantially pure when it is at least 60%, more generally 75% or over 90%, by weight, of the total material in a sample. Thus, for example, a polypeptide that is chemically synthesized or produced by recombinant technology will be generally be substantially free from its naturally

associated components. A nucleic acid molecule may be substantially pure when it is not immediately contiguous with (i.e., covalently linked to) the coding sequences with which it is normally contiguous in the naturally occurring genome of the organism from which the DNA of the invention is derived. A nucleic acid molecule may also be substantially pure when it is isolated from the organism in which it is normally found. A substantially pure compound can be obtained, for example, by extraction from a natural source; by expression of a recombinant nucleic acid molecule encoding a polypeptide compound; or by chemical synthesis. Purity can be measured using any appropriate method such as column chromatography, gel electrophoresis, HPLC, etc.

A "substantially identical" sequence is an amino acid or nucleotide sequence that differs from a reference sequence only by one or more conservative substitutions, as discussed herein, or by one or more non-conservative substitutions, deletions, or insertions located at positions of the sequence that do not destroy the biological function of the amino acid or nucleic acid molecule. Such a sequence can be at least 10%, 20%, 30%, 40%, 50%, 52.5%, 55% or 60% or 75%, or more generally at least 80%, 85%, 90%, or 95%, or as much as 99% or 100% identical at the amino acid or nucleotide level to the sequence used for comparison using, for example, the Align Program (Myers and Miller, CABIOS, 1989, 4:11-17) or FASTA. For polypeptides, the length of comparison sequences may be at least 4, 5, 10, or 15 amino acids, or at least 20, 25, or 30 amino acids. In alternate embodiments, the length of comparison sequences may be at least 35, 40, or 50 amino acids, or over 60, 80, or 100 amino acids. For nucleic acid molecules, the length of comparison sequences may be at least 15, 20, or 25 nucleotides, or at least 30, 40, or 50 nucleotides. In alternate embodiments, the length of comparison sequences may be at least 60, 70, 80, or 90 nucleotides, or over 100, 200, or 500 nucleotides. Sequence identity can be readily measured using publicly available sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wis. 53705, or BLAST software available from the National Library of Medicine, or as described herein). Examples of useful software include the programs Pile-up and PrettyBox. Such software matches similar sequences by assigning degrees of homology to various substitutions, deletions, insertions, and other modifications.

Alternatively, or additionally, two nucleic acid sequences may be “substantially identical” if they hybridize under high stringency conditions. In some embodiments, high stringency conditions are, for example, conditions that allow hybridization comparable with the hybridization that occurs using a DNA probe of at least 500
5 nucleotides in length, in a buffer containing 0.5 M NaHPO₄, pH 7.2, 7% SDS, 1 mM EDTA, and 1% BSA (fraction V), at a temperature of 65°C, or a buffer containing 48% formamide, 4.8x SSC, 0.2 M Tris-Cl, pH 7.6, 1x Denhardt's solution, 10% dextran sulfate, and 0.1% SDS, at a temperature of 42°C. (These are typical conditions for high stringency northern or Southern hybridizations.) Hybridizations may be carried out
10 over a period of about 20 to 30 minutes, or about 2 to 6 hours, or about 10 to 15 hours, or over 24 hours or more. High stringency hybridization is also relied upon for the success of numerous techniques routinely performed by molecular biologists, such as high stringency PCR, DNA sequencing, single strand conformational polymorphism analysis, and in situ hybridization. In contrast to northern and Southern hybridizations,
15 these techniques are usually performed with relatively short probes (e.g., usually about 16 nucleotides or longer for PCR or sequencing and about 40 nucleotides or longer for in situ hybridization). The high stringency conditions used in these techniques are well known to those skilled in the art of molecular biology, and examples of them can be found, for example, in Ausubel et al., Current Protocols in Molecular Biology, John
20 Wiley & Sons, New York, N.Y., 1998, which is hereby incorporated by reference.

The terms “nucleic acid” or “nucleic acid molecule” encompass both RNA (plus and minus strands) and DNA, including cDNA, genomic DNA, and synthetic (e.g., chemically synthesized) DNA. The nucleic acid may be double-stranded or single-stranded. Where single-stranded, the nucleic acid may be the sense strand or the
25 antisense strand. A nucleic acid molecule may be any chain of two or more covalently bonded nucleotides, including naturally occurring or non-naturally occurring nucleotides, or nucleotide analogs or derivatives. By “RNA” is meant a sequence of two or more covalently bonded, naturally occurring or modified ribonucleotides. One example of a modified RNA included within this term is phosphorothioate RNA. By
30 “DNA” is meant a sequence of two or more covalently bonded, naturally occurring or modified deoxyribonucleotides. By “cDNA” is meant complementary or copy DNA produced from an RNA template by the action of RNA-dependent DNA polymerase

(reverse transcriptase). Thus a "cDNA clone" means a duplex DNA sequence complementary to an RNA molecule of interest, carried in a cloning vector.

An "isolated nucleic acid" is a nucleic acid molecule that is free of the nucleic acid molecules that normally flank it in the genome or that is free of the organism in which it is normally found. Therefore, an "isolated" gene or nucleic acid molecule is in some cases intended to mean a gene or nucleic acid molecule which is not flanked by nucleic acid molecules which normally (in nature) flank the gene or nucleic acid molecule (such as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (as in a cDNA or RNA library). In some cases, an isolated nucleic acid molecule is intended to mean the genome of an organism such as a virus. An isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. The term therefore includes, e.g., a genome; a recombinant nucleic acid incorporated into a vector, such as an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other sequences. It also includes a recombinant nucleic acid which is part of a hybrid gene encoding additional polypeptide sequences. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present. Thus, an isolated gene or nucleic acid molecule can include a gene or nucleic acid molecule which is synthesized chemically or by recombinant means. Recombinant DNA contained in a vector are included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. In vivo and in vitro RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleic acid molecules. Such isolated nucleic acid molecules are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences

(e.g., from other species), for gene mapping (e.g., by in situ hybridization with chromosomes), or for detecting expression of the nucleic acid molecule in tissue (e.g., human tissue, such as peripheral blood), such as by Northern blot analysis.

Various genes and nucleic acid sequences of the invention may be recombinant sequences. The term "recombinant" means that something has been recombined, so that when made in reference to a nucleic acid construct the term refers to a molecule that is comprised of nucleic acid sequences that are joined together or produced by means of molecular biological techniques. The term "recombinant" when made in reference to a protein or a polypeptide refers to a protein or polypeptide molecule which is expressed using a recombinant nucleic acid construct created by means of molecular biological techniques. The term "recombinant" when made in reference to genetic composition refers to a gamete or progeny with new combinations of alleles that did not occur in the parental genomes. Recombinant nucleic acid constructs may include a nucleotide sequence which is ligated to, or is manipulated to become ligated to, a nucleic acid sequence to which it is not ligated in nature, or to which it is ligated at a different location in nature. Referring to a nucleic acid construct as "recombinant" therefore indicates that the nucleic acid molecule has been manipulated using genetic engineering, i.e. by human intervention. Recombinant nucleic acid constructs may for example be introduced into a host cell by transformation. Such recombinant nucleic acid constructs may include sequences derived from the same host cell species or from different host cell species, which have been isolated and reintroduced into cells of the host species. Recombinant nucleic acid construct sequences may become integrated into a host cell genome, either as a result of the original transformation of the host cells, or as the result of subsequent recombination and/or repair events.

As used herein, "heterologous" in reference to a nucleic acid or protein is a molecule that has been manipulated by human intervention so that it is located in a place other than the place in which it is naturally found. For example, a nucleic acid sequence from one species may be introduced into the genome of another species, or a nucleic acid sequence from one genomic locus may be moved to another genomic or extrachromosomal locus in the same species. A heterologous protein includes, for example, a protein expressed from a heterologous coding sequence or a protein

expressed from a recombinant gene in a cell that would not naturally express the protein.

By “antisense,” as used herein in reference to nucleic acids, is meant a nucleic acid sequence that is complementary to one strand of a nucleic acid molecule. In some
5 embodiments, an antisense sequence is complementary to the coding strand of a gene, preferably, a SARS virus gene. The preferred antisense nucleic acid molecule is one which is capable of lowering the level of polypeptide encoded by the complementary gene when both are expressed in a cell. In some embodiments, the polypeptide level is lowered by at least 10%, or at least 25%, or at least 50%, as compared to the
10 polypeptide level in a cell expressing only the gene, and not the complementary antisense nucleic acid molecule.

A “probe” or “primer” is a single-stranded DNA or RNA molecule of defined sequence that can base pair to a second DNA or RNA molecule that contains a complementary sequence (the target). The stability of the resulting hybrid molecule
15 depends upon the extent of the base pairing that occurs, and is affected by parameters such as the degree of complementarity between the probe and target molecule, and the degree of stringency of the hybridization conditions. The degree of hybridization stringency is affected by parameters such as the temperature, salt concentration, and concentration of organic molecules, such as formamide, and is determined by methods
20 that are known to those skilled in the art. Probes or primers specific for SARS virus nucleic acid sequences or molecules may vary in length from at least 8 nucleotides to over 500 nucleotides, including any value in between, depending on the purpose for which, and conditions under which, the probe or primer is used. For example, a probe or primer may be 8, 10, 15, 20, or 25 nucleotides in length, or may be at least 30, 40,
25 50, or 60 nucleotides in length, or may be over 100, 200, 500, or 1000 nucleotides in length. Probes or primers specific for SARS virus nucleic acid molecules may have greater than 20-30% sequence identity, or at least 55-75% sequence identity, or at least 75-85% sequence identity, or at least 85-99% sequence identity, or 100% sequence identity to the nucleic acid sequences described herein. In various embodiments of the
30 invention, probes having the sequences: 5'- ATg AAT TAC CAA gTC AAT ggT TAC -3', SEQ ID NO: 160; 5'- gAA gCT ATT CgT CAC gTT Cg-3', SEQ ID NO: 161; 5'- CTg TAg AAA ATC CTA gCT ggA g-3', SEQ ID NO: 162; 5'- CAT AAC CAg TCg

gTA CAg CTA-3', SEQ ID NO: 163; 5'- TTA TCA CCC gCgAAg AAg CT-3', SEQ ID NO: 164; 5'- CTC TAg TTg CATgAC AgC CCT C-3', SEQ ID NO: 165; 5'- TCg TgC gTg gAT TggCTT TgA TgT-3', SEQ ID NO: 166; 5'-ggg TTg ggA CTA TCC TAA gTg TgA-3', SEQ ID NO: 167; 5'-TAA CAC ACA AAC ACC ATC ATC A-3', SEQ ID NO: 168; 5'-ggT Tgg gAC TAT CCT AAg TgT gA-3', SEQ ID NO: 169; 5'-CCA TCA TCA gAT AgA ATC ATC ATA-3', SEQ ID NO: 170; 5'- CCT CTC TTg TTC TTg CTC gCA-3', SEQ ID NO: 171; 5'- TAT AgT gAg CCg CCA CAC Atg-3', SEQ ID NO: 172; 5'-TAACACACAACICCATCATCA-3', SEQ ID NO: 173; 5'-CTAACATGCTTAGGATAATGG-3', SEQ ID NO: 174; 5'-GCCTCTCTTGTTCCTTGCTCGC-3', SEQ ID NO: 175; 5'-CAGGTAAGCGTAAAACTCATC-3', SEQ ID NO: 176; 5'-TACACACCTCAGCGTTG-3', SEQ ID NO: 177; 5'-CACGAACGTGACGAAT-3', SEQ ID NO: 178; 5'-GCCGGAGCTCTGCAGAATTC-3', SEQ ID NO: 179; 5'-CAGGAAACAGCTATGAC TTGCATCACCAGTTGTGCCACCAGGTT-3', SEQ ID NO: 180; 5'-TGTAACACGACGGCCAGTTGATGGGATGGGACTATCCTAAGTGTGA-3', SEQ ID NO: 181; 5'- GCATAGGCAGTAGTTGCATC-3' , SEQ ID NO: 182, as well as sequences amplified by specific combinations of these probes, may be excluded from specific uses according to the invention. Probes can be detectably-labeled, either radioactively or non-radioactively, by methods that are known to those skilled in the art. Probes can be used for methods involving nucleic acid hybridization, such as nucleic acid sequencing, nucleic acid amplification by the polymerase chain reaction, single stranded conformational polymorphism (SSCP) analysis, restriction fragment polymorphism (RFLP) analysis, Southern hybridization, northern hybridization, in situ hybridization, electrophoretic mobility shift assay (EMSA), and other methods that are known to those skilled in the art.

By "complementary" is meant that two nucleic acid molecules, e.g., DNA or RNA, contain a sufficient number of nucleotides that are capable of forming Watson-Crick base pairs to produce a region of double-strandedness between the two nucleic acids. Thus, adenine in one strand of DNA or RNA pairs with thymine in an opposing complementary DNA strand or with uracil in an opposing complementary RNA strand. It will be understood that each nucleotide in a nucleic acid molecule need not form a

matched Watson-Crick base pair with a nucleotide in an opposing complementary strand to form a duplex.

By “vector” is meant a DNA molecule derived, e.g., from a plasmid, bacteriophage, or mammalian or insect virus, or artificial chromosome, that may be used to introduce a polypeptide, for example a SARS virus polypeptide, into a host cell by means of replication or expression of an operably linked heterologous nucleic acid molecule. By “operably linked” is meant that a nucleic acid molecule such as a gene and one or more regulatory sequences (e.g., promoters, ribosomal binding sites, terminators in prokaryotes; promoters, terminators, enhancers in eukaryotes; leader sequences, etc.) are connected in such a way as to permit the desired function e.g. gene expression when the appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequences. A vector may contain one or more unique restriction sites and may be capable of autonomous replication in a defined host or vehicle organism such that the cloned sequence is reproducible. By “DNA expression vector” is meant any autonomous element capable of directing the synthesis of a recombinant peptide. Such DNA expression vectors include bacterial plasmids and phages and mammalian and insect plasmids and viruses. A “shuttle vector” is understood as meaning a vector which can be propagated in at least two different cell types, or organisms, for example vectors which are first propagated or replicated in prokaryotes in order for, for example, subsequent transfection into eukaryotic cells. A “replicon” is a unit that is capable of autonomous replication in a cell and may includes plasmids, chromosomes (e.g., mini-chromosomes), cosmids, viruses, etc. A replicon may be a vector.

A “host cell” is any cell, including a prokaryotic or eukaryotic cell, into which a replicon, such as a vector, has been introduced by for example transformation, transfection, or infection.

An “open reading frame” or “ORF” is a nucleic acid sequence that encodes a polypeptide. An ORF may include a coding sequence having i.e., a sequence that is capable of being transcribed into mRNA and/or translated into a protein when combined with the appropriate regulatory sequences. In general, a coding sequence includes a 5’ translation start codon and a 3’ translation stop codon.

A "leader sequence" is a relatively short nucleotide sequence located at the 5' end of an RNA molecule that acts as a primer for transcription.

A "transcriptional regulatory sequence" "TRS" or "intergenic sequence" is a nucleotide sequence that lies upstream of an open reading frame (ORF) and serves as a
5 template for the reassociation of a nascent RNA strand-polymerase complex.

A "frameshift mutation" is caused by a shift in a open reading frame, generally due to a deletion or addition of at least one nucleotide, such that an alternative polypeptide is ultimately translated.

By "detectably labeled" is meant any means for marking and identifying the
10 presence of a molecule, e.g., an oligonucleotide probe or primer, a gene or fragment thereof, a cDNA molecule, a polypeptide, or an antibody. Methods for detectably-labeling a molecule are well known in the art and include, without limitation, radioactive labeling (e.g., with an isotope such as ³²P or ³⁵S) and nonradioactive labeling such as, enzymatic labeling (for example, using horseradish peroxidase or
15 alkaline phosphatase), chemiluminescent labeling, fluorescent labeling (for example, using fluorescein), bioluminescent labeling, antibody detection of a ligand attached to the probe, or detection of double-stranded nucleic acid. Also included in this definition is a molecule that is detectably labeled by an indirect means, for example, a molecule that is bound with a first moiety (such as biotin) that is, in turn, bound to a second
20 moiety that may be observed or assayed (such as fluorescein-labeled streptavidin). Labels also include digoxigenin, luciferases, and aequorin.

A "peptide," "protein," "polyprotein" or "polypeptide" is any chain of two or more amino acids, including naturally occurring or non-naturally occurring amino acids or amino acid analogues, regardless of post-translational modification (e.g.,
25 glycosylation or phosphorylation). An "polyprotein", "polypeptide", "peptide" or "protein" of the invention may include peptides or proteins that have abnormal linkages, cross links and end caps, non-peptidyl bonds or alternative modifying groups. Such modified peptides are also within the scope of the invention. The term
"modifying group" is intended to include structures that are directly attached to the
30 peptidic structure (e.g., by covalent coupling), as well as those that are indirectly attached to the peptidic structure (e.g., by a stable non-covalent association or by covalent coupling to additional amino acid residues, or mimetics, analogues or

derivatives thereof, which may flank the core peptidic structure). For example, the modifying group can be coupled to the amino-terminus or carboxy-terminus of a peptidic structure, or to a peptidic or peptidomimetic region flanking the core domain. Alternatively, the modifying group can be coupled to a side chain of at least one amino acid residue of a peptidic structure, or to a peptidic or peptido-mimetic region flanking the core domain (e.g., through the epsilon amino group of a lysyl residue(s), through the carboxyl group of an aspartic acid residue(s) or a glutamic acid residue(s), through a hydroxy group of a tyrosyl residue(s), a serine residue(s) or a threonine residue(s) or other suitable reactive group on an amino acid side chain). Modifying groups covalently coupled to the peptidic structure can be attached by means and using methods well known in the art for linking chemical structures, including, for example, amide, alkylamino, carbamate or urea bonds.

A "polyprotein" is the polypeptide that is initially translated from the genome of a plus-stranded RNA virus, for example, a SARS virus. Accordingly, a polyprotein has not been subjected to post-translational processing by proteolytic cleavage into its processed protein products, and therefore, retains its cleavage sites. In some embodiments of the invention, the protease cleavage sites of a polyprotein may be modified, for example, by amino acid substitution, to result in a polyprotein that is incapable of being cleaved into its processed protein products.

An antibody "specifically binds" or "selectively binds" an antigen when it recognizes and binds the antigen, but does not substantially recognize and bind other molecules in a sample, having for example an affinity for the antigen which is 10, 100, 1000 or 10000 times greater than the affinity of the antibody for another reference molecule in a sample. A "neutralizing antibody" is an antibody that selectively interferes with any of the biological activities of a SARS virus polypeptide or polyprotein, for example, replication of the SARS virus, or infection of host cells. A neutralizing antibody may reduce the ability of a SARS virus polypeptide to carry out its specific biological activity by about 50%, or by about 70%, or by about 90% or more, or may completely abolish the ability of a SARS virus polypeptide to carry out its specific biological activity. Any standard assay for the biological activity of any SARS virus polypeptide, for example, assays determining expression levels, ability to infect host cells, or ability to replicate DNA, including those assays described herein or

known to those of skill in the art, may be used to assess potentially neutralizing antibodies that are specific for SARS virus polypeptides.

A "signal sequence" is a sequence of amino acids that may be identified, for example by homology or biological activity to a peptide sequence with the known
5 function of targeting a polypeptide to a particular region of the cell. A signal sequence or signal peptide may be a peptide of any length, that is capable of targeting a polypeptide to a particular region of the cell. In some embodiments, the signal sequence may direct the polypeptide to the cellular membrane so that the polypeptide may be secreted. In alternate embodiments, the signal sequence may direct the
10 polypeptide to an intracellular compartment or organelle, such as the Golgi apparatus, or to the surface of a virus, such as the SARS virus. In alternate embodiments, a signal sequence may range from about 13 or 15 amino acids in length to about 60 amino acids in length.

A "transmembrane protein" is an amphipathic protein having a hydrophobic
15 region ("transmembrane domain") that spans the lipid bilayer of the cell membrane from the cytoplasm to the cell surface, or spans the viral envelope, interspersed between hydrophilic regions on both sides of the membrane. The number of hydrophobic regions in an amphipathic protein is often proportional to the number of times that proteins spans the lipid bilayer. Thus, a single transmembrane protein spans
20 the lipid bilayer once, and has a single transmembrane domain, while a multi-transmembrane protein spans the lipid bilayer multiple times. Multi-transmembrane proteins may enable virus entry into a host cell, or act to initiate transduction of a signal from the cell surface to the interior of the cell, for example, by a conformational change upon ligand binding. A "transmembrane anchor" is a transmembrane domain that
25 maintains a polypeptide in its position in the cell membrane or viral envelope and is generally hydrophobic. A transmembrane anchor may generally be in the structure of an alpha helix, i.e., a "transmembrane helix". Multi-transmembrane proteins may have multiple transmembrane alpha-helices.

A "nuclear localization signal" is an amino acid sequence that permits the entry
30 of a polypeptide into the nucleus of a cell through nuclear pores. A nuclear localization signal generally has a cluster of positively charged residues, for example, lysines. A "lysine-rich sequence" is a sequence having at least two contiguous lysine residues, or

at least three contiguous lysine residues. In some embodiments, a lysine-rich sequence may be a nuclear localization signal.

An "ATP binding domain" is a consensus domain that is found in many ATP or GTP-binding proteins, and that forms a flexible loop (P-loop) between alpha-helical and beta pleated sheet domains. The general consensus for an ATP binding domain may be (A or G)-XXXXGK-(S or T).

A "RNA binding protein" is a protein that is capable of binding to a RNA molecule (see, for example, "RNA Binding Proteins: New Concepts in Gene Regulation" 1st ed, eds. K. Sandberg and S.E. Mulroney, Kluwers Academic Publishers, 2001). RNA binding proteins may contain common structural features such as arginine-rich tracts, for example, arginines alternating with aspartates, serines, or glycines, or zinc finger regions. RNA binding proteins may also have a common ribonucleotide sequence domain. RNA binding proteins are believed to play diverse roles in modulating post-transcriptional gene expression.

An "immune response" includes, but is not limited to, one or more of the following responses in a mammal: induction of antibodies, B cells, T cells (including helper T cells, suppressor T cells, cytotoxic T cells, $\gamma\delta$ T cells) directed specifically to the antigen(s) in a composition or vaccine, following administration of the composition or vaccine. An immune response to a composition or vaccine thus generally includes the development in the host mammal of a cellular and/or antibody-mediated response to the composition or vaccine of interest. In general, the immune response will result in prevention or reduction of infection by a SARS virus.

An "immunogenic fragment" of a polypeptide or nucleic acid molecule refers to an amino acid or nucleotide sequence that elicits an immune response. Thus, an immunogenic fragment may include, without limitation, any portion of any of the SARS virus sequences described herein, or a sequence substantially identical thereto, that includes one or more epitopes (the antigenic determinant i.e., site recognized by a specific immune system cell, such as a T cell or a B cell). An "epitope" may include amino acids in a spatial orientation that they are non-contiguous in the amino acid sequence but are near each other due to the three dimensional conformation of the polypeptide. A epitope may include at least 3, 5, 8, or 10 or more amino acids. Immunogenic fragments or epitopes may be identified using standard methods known

to those of skill in the art, such as epitope mapping techniques or antigenicity or hydropathy plots using, for example, the Omega version 1.0 program from Oxford Molecular Group (see, for example, U. S. Patent No. 4,708,871). Immunogenic fragments or epitopes may also be identified using methods for determining three dimensional molecule structure such as X-ray crystallography or nuclear magnetic resonance.

A "sample" may be a tissue biopsy, amniotic fluid, cell, blood, serum, plasma, urine, stool, sputum, conjunctiva, or any other specimen, or any extract thereof, obtained from a patient (human or animal), test subject, or experimental animal. A "sample" may also be a cell or cell line created under experimental conditions, and constituents thereof (such as cell culture supernatants, cell fractions, infected cells, etc.). The sample may be analyzed to detect the presence of a SARS virus gene, genome, polypeptide, nucleic acid molecule or virion, or to detect a mutation in a SARS virus gene, expression levels of a SARS virus gene or polypeptide, or the biological function of a SARS virus polypeptide, using methods that are known in the art. For example, methods such as sequencing, single-strand conformational polymorphism (SSCP) analysis, or restriction fragment length polymorphism (RFLP) analysis of PCR products derived from a sample can be used to detect a mutation in a SARS virus gene; ELISA or western blotting can be used to measure levels of SARS virus polypeptide or antibody affinity; northern blotting can be used to measure SARS mRNA levels, or PCR can be used to measure the level of a SARS virus nucleic acid molecule.

Other features and advantages of the invention will be apparent from the following description of the drawings and the invention, and from the claims.

Brief Description of the Drawings

Figures 1A-D show phylogenetic analyses of SARS proteins. Unrooted phylogenetic trees were generated by clustalw (Thompson, J. D. et al., *Nucleic Acids Res* 22, 4673-80, Nov 11, 1994) bootstrap analysis using 1000 iterations. Genbank accessions for protein sequences are as follows: Figure 1A: Replicase 1A: BoCov (Bovine Coronavirus):AAL40396, 229E (Human Coronavirus):NP_07355, MHV (Mouse Hepatitis Virus):NP_045298, AIBV (Avian Infectious bronchitis

virus):CAC39113, TGEV (Transmissible Gastroenteritis Virus): NP_058423. Figure 1B: Matrix Glycoprotein: PHEV (Porcine hemagglutinating encephalomyelitis virus):AAL80035, BoCov (Bovine Coronavirus):NP_150082, AIBV & AIBV2 (Avian infectious bronchitis virus): AAF35863 & AAK83027, MHV (Mouse hepatitis virus):AAF36439, TGEV (Transmissible gastroenteritis virus):NP_058427, 229E & OC43 (Human Coronavirus): NP_073555 & AAA45462, FCV (Feline coronavirus):BAC01160. Figure 1C: Nucleocapsid: MHV (Mouse hepatitis virus):P18446, BoCov (Bovine coronavirus):NP_150083, AIBV (Avian infectious bronchitis virus):AAK27162, FCV (Feline coronavirus):CAA74230, PTGV (Porcine transmissible gastroenteritis virus): AAM97563, 229E & OC43 (Human coronavirus):NP_073556 & P33469, PHEV (porcine hemagglutinating encephalomyelitis virus):AAL80036, TCV (Turkey coronavirus):AAF23873. Figure 1D: S (Spike) Protein: BoCov (Bovine coronavirus):AAL40400, MHV (Mouse hepatitis virus): P11225, OC43 & 229E (Human coronavirus):S44241 & AAK32191, PHEV (Porcine hemagglutinating encephalomyelitis virus):AAL80031, PRC (Porcine respiratory coronavirus):AAA46905, PEDV (Porcine epidemic diarrhea virus):CAA80971, CCov (Canine coronavirus):S41453, FICV (Feline infectious peritonitis virus):BAA06805, AIBV (Avian infectious bronchitis virus):AAO34396.

Figure 2 shows a schematic representation of the ORFs and s2m motif in the 29,736-base SARS virus genome.

Figures 3A-P show nucleotide sequences of the 29,736-base genome of the SARS virus (SEQ ID NOs: 1 and 2).

Figure 4 shows an alignment of the s2m regions from Avian infectious bronchitis virus (AIBV; SEQ ID NO: 32) and equine rhinovirus serotype 2 (ERV-2; SEQ ID NO: 31) with the 3' untranslated region (UTR; SEQ ID NO: 18) of the SARS virus (TOR2). The conserved areas in the s2m region are indicated by asterisks.

Figure 5 shows the amino acid sequence of the SARS virus S (Spike) Glycoprotein (SEQ ID NO: 33).

Figure 6 shows the amino acid sequence of the SARS virus M (Matrix) Glycoprotein (SEQ ID NO: 34).

Figure 7 shows the amino acid sequence of the SARS virus E (Small envelope) protein (SEQ ID NO: 35).

Figure 8 shows the amino acid sequence of the SARS virus N (Nucleocapsid) Protein (SEQ ID NO: 36).

Figure 9 shows an alignment of the matrix glycoprotein M from the SARS virus (Tor2_M or ORF5; SEQ ID NO: 34) and various other matrix glycoproteins (SEQ ID NOs: 37-43). Asterisks (*) indicate percentage identity to the SARS matrix protein as calculated by Align (Myers and Miller, CABIOS (1989) 4:11-17).

Figures 10A-B show an alignment of the nucleocapsid protein N from the SARS virus (Tor2_N; SEQ ID NO: 36) and various other nucleocapsid proteins (SEQ ID NOs: 44-52). Asterisks (*) indicate percentage identity to the SARS nucleocapsid protein calculated by Align (Myers and Miller, CABIOS (1989) 4:11-17). **Figures 11A-K** show the nucleotide sequence of the 29,751-base genome of the SARS virus (SEQ ID NO: 15).

Figure 12 shows a schematic representation of the ORFs and s2m motif in the 29,751-base SARS virus genome.

Figures 13A-D show phylogenetic analyses of SARS proteins. Unrooted phylogenetic trees were generated by clustalw 1.74 (J. D. Thompson, D. G. Higgins, T. J. Gibson, Nucleic Acids Res 22, 4673-80 (Nov 11, 1994) using the BLOSUM comparison matrix and a bootstrap analysis of 1000 iterations. Numbers indicate bootstrap replicates supporting each node. Phylogenetic trees were drawn with the Phylip Drawtree program 3.6a3 (Felsenstein, J. 1993. PHYLIP (Phylogeny Inference Package) version 3.5c. Distributed by the author. Department of Genetics, University of Washington, Seattle). Branch lengths indicate the number of substitutions per residue. Genbank accessions for protein sequences: A: Replicase 1A: BoCoV (Bovine Coronavirus):AAL40396, HCoV-229E (Human Coronavirus):NP_07355, MHV (Mouse Hepatitis Virus):NP_045298, IBV (Avian Infectious bronchitis virus):CAC39113, TGEV (Transmissible Gastroenteritis Virus): NP_058423. B: Membrane Glycoprotein: PHEV (Porcine hemagglutinating encephalomyelitis virus):AAL80035, BoCoV (Bovine Coronavirus):NP_150082, IBV & IBV2 (Avian infectious bronchitis virus): AAF35863 & AAK83027, MHV (Mouse hepatitis virus):AAF36439, TGEV (Transmissible gastroenteritis virus):NP_058427, HCoV-229E & HCoV-OC43 (Human Coronavirus): NP_073555 & AAA45462, FCoV (Feline coronavirus):BAC01160. C: Nucleocapsid: MHV (Mouse hepatitis virus):P18446,

BoCoV (Bovine coronavirus):NP_150083, IBV 1 & 2 (Avian infectious bronchitis virus): AAK27162 & NP_040838, FCoV (Feline coronavirus):CAA74230, PTGV (Porcine transmissible gastroenteritis virus): AAM97563, HCoV-229E & HCoV-OC43 (Human coronavirus):NP_073556 & P33469, PHEV (porcine hemagglutinating encephalomyelitis virus):AAL80036, TCV (Turkey coronavirus):AAF23873. D: S (Spike) Protein: BoCoV (Bovine coronavirus):AAL40400, MHV (Mouse hepatitis virus): P11225, HCoV-OC43 & HCoV-229E (Human coronavirus):S44241 & AAK32191, PHEV (Porcine hemagglutinating encephalomyelitis virus):AAL80031, PRCoV (Porcine respiratory coronavirus):AAA46905, PEDV (Porcine epidemic diarrhea virus):CAA80971, CCoV (Canine coronavirus):S41453, FIPV (Feline infectious peritonitis virus):BAA06805, IBV (Avian infectious bronchitis virus):AAO34396.

Figures 14A-F show an alignment of the spike glycoprotein S from the SARS virus (Tor2_S; SEQ ID NO: 33) and various other spike glycoproteins (SEQ ID NOs: 53-62). Asterisks (*) indicate percentage identity to the SARS spike protein as calculated by Align (Myers and Miller, CABIOS (1989) 4:11-17).

Figure 15 shows an alignment between the SARS virus Small envelope protein E (TOR2_E; SEQ ID NO: 35) and the Envelope protein (Protein 4) (X1 protein) (ORF 3) from Porcine transmissible gastroenteritis coronavirus (strain Purdue).Swissprot accession number P09048 (PGV; SEQ ID NO: 63), as calculated by FASTA (<http://www.ebi.ac.uk/fasta33/>).

Figures 16A-B show the amino acid sequence of the SARS virus Replicase 1A protein (SEQ ID NO: 64).

Figure 17 shows the amino acid sequence of the SARS virus Replicase 1B protein (SEQ ID NO: 65).

Figure 18 shows the amino acid sequence of ORF3 of SARS virus (SEQ ID NO: 66).

Figure 19 shows the amino acid sequence of ORF4 of SARS virus (SEQ ID NO: 67).

Figure 20 shows the amino acid sequence (SEQ ID NO: 68) of ORF6 (nucleotides 27059-27247 of the 29,736-base genome sequence) or ORF 7 (nucleotides 27,074-27,265 of the 29,751-base genome sequence) of SARS virus.

Figure 21 shows the amino acid sequence (SEQ ID NO: 69) of ORF7 (nucleotides 27258-27623 of the 29,736-base genome sequence) or ORF 8 (nucleotides 27,273-27,641 of the 29,751-base genome sequence), of SARS virus.

Figure 22 shows the amino acid sequence (SEQ ID NO: 70) of ORF8 (nucleotides 27623-27754 of the 29,736-base genome sequence) or ORF9 8 (nucleotides 27,638-27,772 of the 29,751-base genome sequence) of SARS virus.

Figure 23 shows the amino acid sequence (SEQ ID NO: 71) of ORF9 (nucleotides 27764-27880 of the 29,736-base genome sequence) or ORF10 (nucleotides 27,779-27,898 of the 29,751-base genome sequence) of SARS virus.

Figure 24 shows the amino acid sequence (SEQ ID NO: 72) of ORF10 (nucleotides 27849-28100 of the 29,736-base genome sequence) or ORF11 (nucleotides 27,864-28118 of the 29,751-base genome sequence) of SARS virus.

Figure 25 shows the amino acid sequence of ORF13 of SARS virus (SEQ ID NO: 73).

Figure 26 shows the amino acid sequence of ORF14 of SARS virus (SEQ ID NO: 74).

Figure 27 shows an alignment of the secreted region of the SARS virus ORF 10 of the 29,751-base genome sequence (sars) with the conotoxin from *Conus ventricosus* (conotoxin). Sequence identity is indicated by asterisks and sequence homology is indicated by dots.

Detailed Description of the Invention

In general, the invention provides nucleic acid molecules, polypeptides, and other reagents derived from a SARS virus, as well as methods of using such nucleic acid molecules, polypeptides, and other reagents.

The genome sequence (Figures 3A-P, 11A-K, SEQ ID NOs: 1, 2, and 15) reveals that the SARS coronavirus is only moderately related to other known coronaviruses, including two human coronaviruses, OC43 and 229E. Thus, the SARS virus is a previously unknown virus. The 5' end of the SARS genome contains a 5' leader sequence (Table 1; SEQ ID NO: 3) with sequence similarity to the highly conserved coronavirus core leader sequence, 5'-CUAAAC-3 (SEQ ID NO: 75;

Sawicki, S. G., et al., *Adv Exp Med Biol* 440, 215-9, 1998; Lai, M. M. and D. Cavanagh, *Adv Virus Res* 48, 1-100, 1997). Transcriptional regulatory sequences (TRSs) were identified upstream of all open reading frames (ORFs) (Tables 1 and 2; SEQ ID NOs: 3-13 and 20-30). ORF9 and ORF10 of the 29,736-base SARS genome (ORF 10 and ORF 11 of the 29,751 base genome) overlap by 12 amino acids, and have matches to the TRS consensus in close proximity to their respective initiating methionine codons.

The 3' UTR sequence (SEQ ID NO: 18) of SARS virus contains a s2m region having the sequence ACATTTTCATCGAGGCCACGCGGAGTACGAT CGAGGGTACAGTGAAT; SEQ ID NO: 16) that includes a conserved, discontinuous 32 base-pair s2m motif. The conserved 32 base-pair motif is a universal feature of astroviruses that has also been identified in avian coronavirus (AIBV) and the ERV-2 equine rhinovirus. This motif has been identified by Jonassen C.M. et al. (*J Gen Virol* 1998 Apr;79 (Pt 4):715-8) as GCCGNGGCCACGC(G/C) GAGTA(C/G)GANC GAGGGTACAG(G/C) (SEQ ID NO: 19), where N is generally not part of the conserved motif, and can be any nucleotide. The region corresponding to the 32 base-pair motif in SARS virus includes the sequence: CGAGGCCACGCGGAGTACGATCGAGGGTACAG (SEQ ID NO: 17), and spans positions 29590-29621 of the 29,751 base genome. Figure 4 shows an alignment of the s2m regions from Avian infectious bronchitis virus (AIBV; SEQ ID NO: 32) and equine rhinovirus serotype 2 (ERV-2; SEQ ID NO: 31), as defined in Jonassen C.M. et al. (*J Gen Virol* 1998 Apr;79 (Pt 4):715-8), with the entire 3' untranslated region (UTR) of the SARS virus (TOR2) (SEQ ID NO: 18).

Table 1. Listing of the transcription regulatory sequences of the 29,736-base SARS genome, showing the nucleotide position (base) and associated open-reading frames (ORF). An asterisk (*) indicates consensus sequence.

5	Base	ORF	TRS Sequence	
	45	Leader	TCTCTAAACGAACTTTAAATCTGTG	(SEQ ID NO: 3)
	21464	S	CAACTAAACGAACATG	(SEQ ID NO: 4)
	25238	ORF3	CACATAAACGAACTTATG	(SEQ ID NO: 5)
	26089	E	TGAGTACGAACTTATG	(SEQ ID NO: 6)
10	26326	M	GGTCTAAACGAACTAACT 40 ATG	(SEQ ID NO: 7)
	26986	ORF6	AACTATAAATT 62 ATG	(SEQ ID NO: 8)
	27244	ORF7	TCCATAAACGAACATG	(SEQ ID NO: 9)
	27575	ORF8	TGCTCTA---GTATTTTAAATACTTTG 24 ATG	(SEQ ID NO: 10)
	27751	ORF9	AGTCTAAACGAACATG	(SEQ ID NO: 11)
15	27837	ORF10	CTAATAAACCTCATG	(SEQ ID NO: 12)
	28084	N	TAAATAAACGAACAAATTAAATG	(SEQ ID NO: 13)

Table 2. Listing of the transcription regulatory sequences of the 29,751-base SARS genome, showing the nucleotide position (base), associated open-reading frames (ORF), and identified transcription regulatory sequences. Numbers in parentheses within the alignment indicate distance to the putative initiating codon. The conserved core sequence is indicated in bold in the putative leader sequence. Contiguous sequences identical to region of the leader sequence containing the core sequence are shaded. No putative TRSs were detected for ORFs 4, 13 and 14, although ORF 13 may share the TRS associated with the N protein.

	Base	ORF	TRS Sequence	
10	60	Leader	UCUC UAAACGAACUUUAAAAUCUGUG (SEQ ID NO: 20)	
	21479	S (Spike)	CAACUAAACGAACA AUG (SEQ ID NO: 21)	
	25252	ORF3	CACAUAAACGAACUUA AUG (SEQ ID NO: 22)	
	26104	Envelope	UGAGUACGAACUUA AUG (SEQ ID NO: 23)	
	26341	M	GGUCUAAACGAACUAA CU (40) AUG (SEQ ID NO: 24)	
15	27001	ORF7	AACUAUAAAUU (62) AUG (SEQ ID NO: 25)	
	27259	ORF8	UCCAUA AAACGAACA AUG (SEQ ID NO: 26)	
	27590	ORF9	UGCUCUA---GUAUUUUUAAUACU UUG (24) AUG (SEQ ID NO: 27)	
	27766	ORF10	AGUCUAAACGAACA AUG (SEQ ID NO: 28)	
	27852	ORF11	CUAAUAAACCUCA AUG (SEQ ID NO: 29)	
20	28099	NUCLEOCAPSID	UAAAUAAACGAACAAAUU AAAAUG (SEQ ID NO: 30)	

The coding potentials of the 29,736-base and 29,751-base genomes are depicted in Figures 2 and 12, respectively. Open reading frames (ORFs) include the Replicase 1a and 1b translation products, the Spike glycoprotein, the small Envelope protein, the Membrane and the Nucleocapsid protein. Construction of unrooted phylogenetic trees using this set of known proteins from representatives of the three known coronaviral groups reveals that the proteins encoded by the SARS virus do not readily cluster more closely with any known group than with any other (Figures 1A-D and 13A-D). In addition, nine novel ORFs have been analyzed.

The Replicase 1a ORF located at nucleotides 250-13395 of the 29,736-base genome, and nucleotides 265-13,398 of the 29,751-base genome, and replicase 1b ORF located at nucleotides 13395-21467 of the 29,736-base genome, and nucleotides 13,398 – 21,485 of the 29,751-base genome, occupy 21.2 kb of the SARS virus genome (Figures 2 and 12). These genes encode a number of proteins that are produced by proteolytic cleavage of a large polyprotein (Ziebuhr, J. et al., *J Gen Virol* 81, 853-79,

Apr, 2000). A frame shift mutation interrupts the protein-coding region, separating the 1a and 1b open-reading frames. The proteins encoded by the Replicase 1a and 1b ORFs are depicted in Figures 16A-B and 17, SEQ ID NOs: 64 and 65).

The Spike glycoprotein (S) (E2 glycoprotein gene; Figures 2 and 12; nucleotides 21477 to 25241 of the 29,736-base genome, and nucleotides 21,492 to 25,259 of the 29,751-base genome) encodes a surface projection glycoprotein precursor of about 1,255 amino acids in length (Figure 5; SEQ ID NO: 33), which may be significant in the virulence of the SARS virus. Mutations in this gene are correlated with altered pathogenesis and virulence in other coronaviruses (B. N. Fields et al., *Fields virology* (Lippincott Williams & Wilkins, Philadelphia, ed. 4th, 2001). In other coronaviruses, the mature spike protein is inserted in the viral envelope with the majority of the protein exposed on the surface of the particles. Three molecules of the Spike protein form the characteristic peplomers or corona-like structures of this virus family. Analysis of the spike glycoprotein with SignalP (Nielson, H. et al., *Prot Engineer.* 10:1-6 (1997) indicates a signal peptide (MFIFLLFLTLTSG; SEQ ID NO: 76)(probability 0.996) with cleavage between residues 13 and 14. TMHMM (Sonnhammer, E. L. et al., *Proc Int Conf Intell Syst Mol Biol* 6, 175-82 (1998)) indicates a transmembrane domain near the C-terminal end (WYVWLGFIAGLIAIVMTILLCC; SEQ ID NO: 183). Together these data indicate a type I membrane protein with N-terminus and the majority of the protein (residues 14-1195) on the outside of the cell-surface or virus particle, which may be responsible for binding to a cellular receptor. The SARS virus Spike glycoprotein has limited sequence identity to other, known Spike glycoproteins (Figures 14A-F).

ORF 3 (Figures 2 and 12; nucleotides 25253-26074 of the 29,736-base genome and nucleotides 25,268 - 26,092 of the 29,751-base genome) encodes a protein of 274 amino acids (Figure 18; SEQ ID NO: 66) that lacks significant similarities to any known protein when analyzed with BLAST (Altschul, S. F. et al., *Nucleic Acids Res* 25, 3389-402, Sep 1, 1997), FASTA (Pearson, W. R. and D. J. Lipman, *Proc Natl Acad Sci USA* 85, 2444-8, Apr, 1988) or PFAM (Bateman, A. et al., *Nucleic Acids Res* 30, 276-80, Jan 1, 2002). Analysis of the N-terminal 70 amino acids with SignalP indicates the existence of a signal peptide (MDLFMRFFTLRSITAQ; SEQ ID NO: 184) and a cleavage site (probability 0.540). Both TMPred (Hofman, K. and W. Stoffel, *Biol.*

Chem. Hoope-Seyler 374, 166 (1993) and TMHMM indicate three trans-membrane regions spanning approximately residues 34-56 (TIPLQASLPFGWL VIGVAFLAVF, SEQ ID NO: 77), 77-99 (FQFICNLLLLFVTIYSHLLL VAA, SEQ ID NO: 78), and 103-125 (AQFLYLYALIYFLQCINACRIIM, SEQ ID NO: 79). Both TMpred and

5 TMHMM indicate that the C-terminus and a large 149 amino acid domain is located inside the viral or cellular membrane. The C-terminal (interior) region of the protein, corresponding to about amino acids 124-274

(MRCWLCWKCKSKNPLLYDANYFVCWHTHNYDYCIPYNSVTDTIVVTEGDGI
STPKLKEDYQIGGYSEDRHSGVKDYVVVHGYFTEVYYQLESTQITTTDTGIENAT
10 FFIFNKLVDPPNVQIHTIDGSSGVANPAMDPIYDEPTTTTSVPL; SEQ ID NO:
185) may encode a protein domain with ATP-binding properties (PD037277).

ORF 4 (Figure 12; nucleotides 25,689 - 26,153 of the 29,751-base genome) encodes a predicted protein of 154 amino acids (Figure 19; SEQ ID NO: 67). This ORF overlaps entirely with ORF 3 and the E protein. ORF4 may be expressed from the

15 ORF mRNA using an internal ribosomal entry site. BLAST analyses failed to identify matching sequences. Analysis with TMPred predicts a single transmembrane helix, amino acids 1-20 MMPTTLFAGTHITMTTVYHI, SEQ ID NO: 186.

The small envelope protein E (Figures 2 and 12; nucleotides 26102-26329 of the 29,736-base genome and nucleotides 26,117 - 26,347, ORF 5, of the 29,751-

20 genome) encodes a protein of 76 amino acids (Figure 7; SEQ ID NO: 35). BLAST and FASTA comparisons indicate that the protein, while novel, is homologous to multiple envelope proteins (alternatively known as small membrane proteins) from several coronaviruses. An alignment of the SARS virus E protein with the envelope protein of Porcine transmissible gastroenteritis coronavirus indicates approximately 28%

25 sequence identity between the two proteins over a 61 amino acid overlap, as calculated by FASTA (Figure 15). PFAM analysis of the protein indicates that the small envelope protein E is a member of the NS3_EnvE protein family. InterProScan (R. Apweiler et al., *Nucleic Acids Res* 29, 37-40, Jan 1, 2001; Zdobnov, E. M. and R. Apweiler, *Bioinformatics* 17, 847-8, Sep, 2001) analysis indicates that the protein is a component

30 of the viral envelope, and homologs of it are found in other viruses, including gastroenteritis virus and murine hepatitis virus. SignalP analysis indicates the presence of a transmembrane anchor (probability 0.939). TMpred analysis indicates a similar

transmembrane anchor at positions 17-34 (VLLFLAFVVFLVTLAIL, SEQ ID NO: 80), which is consistent with the known association of homologous proteins with the viral envelope. TMHMM indicates a type II membrane protein with the majority of the 46 residue C terminus hydrophilic domain (

5 TALRLCAYCCNIVNVSLVKPTVYVYSRVKNLNSSEGVPDLLV; SEQ ID NO: 187) located on the surface of the viral particle. The E protein may be important for viral replication.

The Matrix glycoprotein M (Figures 2 and 12; nucleotides 26383-27045 of the 29,736-base genome and nucleotides 26,398 - 27,063, ORF 6, of the 29,751-genome) encodes a protein of 221 amino acids (Figure 6; SEQ ID NO: 34). BLAST and FASTA analysis of the protein, while novel, reveals homologies to coronaviral matrix glycoproteins (Figure 9). The association of the spike glycoprotein (S) with the matrix glycoprotein (M) may be an essential step in the formation of the viral envelope and in the accumulation of both proteins at the site of virus assembly. Analysis of the amino acid sequence with SignalP indicates a signal sequence (probability 0.932), located at approximately residues 1-39

(MADNGTITVEELKQLLEQWNLVIGFLFLAWIMLLQFAYS; SEQ ID NO: 188) that is unlikely to be cleaved. TMHMM and TMPred analysis both indicate the presence of three trans-membrane helices, located at approximately residues 15-37

20 (LLEQWNLVIGFLFLAWIMLLQFA; SEQ ID NO: 81), 50-72

(LVFLWLLWPVTLACFVLAAYRI; SEQ ID NO: 82) and 77-99

(GGIAIAMACIVGLMWLSYFVASF; SEQ ID NO: 83), with the 121 amino acid hydrophilic domain on the inside of the virus particle, where it may interact with nucleocapsid. The hydrophilic domain may run from approximately amino acids

25 PLRGITVTRPLMESELVIGAVIIRGHLRMAGHSLGRCDIKDLPKEITVATSRTLS
YYKLGASQRVGTDSGFAAYNRYRIGNYKLNTDHAGSNDNIALLVQ (SEQ ID
NO: 189) i.e. approximately amino acids 95 or 99 to 221 of SEQ ID NO: 34. PFAM analysis reveals a match to PFAM domain PF01635, and alignments to 85 other sequences in the PFAM database bearing this domain, which is indicative of the
30 coronavirus matrix glycoprotein.

ORF6 (Figure 2; nucleotides 27059-27247 of the 29,736-base genome sequence) or ORF 7 (Figure 12; nucleotides 27,074-27,265 of the 29,751-base genome

sequence) encodes a protein of 63 amino acids (Figure 20; SEQ ID NO: 68). TMpred analysis indicates a trans-membrane helix located between residues 3 or 4 and 22 (HLVDFQVTIAEILIIIMRTF; SEQ ID NO: 84), with the N-terminus located outside the viral particle.

5 Similarly, the gene encoding ORF7 (Figure 2; nucleotides 27258-27623 of the 29,736-base genome sequence) or ORF 8 (Figure 12; nucleotides 27,273-27,641 of the 29,751-base genome sequence), encoding a protein of 122 amino acids (Figure 21; SEQ ID NO: 69), has no significant BLAST or FASTA matches to known proteins.

Analysis of this sequence with SignalP indicates a cleaved signal sequence

10 (MKIILFLTLIVFTSC; SEQ ID NO: 85) (probability 0.995), with the cleavage site located between residues 15 and 16. TMpred and TMHMM analysis also indicates a trans-membrane helix located approximately at residues 99-117

(SPLFLIVAALVFLILCFTI; SEQ ID NO: 86). Together these data indicate that this protein is a type I membrane protein with the major hydrophilic domain of the protein

15 (residues 16-98; ELYHYQECVRGTTVLLKEPCP

SGTYEGNSPFHPLADNKFALTCTSTHFAFACADGTRHTYQLRARSVSPKLFIRQ
EEVQQELY; SEQ ID NO: 87) and the amino-terminus is oriented inside the lumen of the ER/Golgi, or on the surface of the cell membrane or virus particle, depending on the membrane localization of the protein.

20 ORF8 (Figure 2; nucleotides 27623-27754 of the 29,736-base genome sequence) or ORF9 (Figure 12; nucleotides 27,638-27,772 of the 29,751-base genome sequence), encodes a protein of 44 amino acids (Figure 22; SEQ ID NO: 70). FASTA analysis of this sequence revealed some weak similarities (37% identity over a 35 amino acid overlap) to Swiss-Prot accession Q9M883, annotated as a putative sterol-C5

25 desaturase. A similarly weak match to a hypothetical *Clostridium perfringens* protein (Swiss-Prot accession CPE2366) was also detected. TMpred indicated a single strong trans-membrane helix FYLCFLAFLFLVLIMLIIFWFS, SEQ ID NO: 190, with little preference for alternate models in which the N-terminus was located inside or outside the particle.

30 Similarly ORF9 (Figure 2; nucleotides 27764-27880 of the 29,736-base genome sequence) or ORF10 (Figure 12; nucleotides 27,779-27,898 of the 29,751-base genome sequence) encoding a protein of 39 amino acids (Figure 23; SEQ ID NO: 71), exhibited

no significant matches in BLAST and FASTA searches but encodes a trans-membrane helix LLIVLTCISLCSCICTVVQ (SEQ ID NO: 191) by TMPred, with the N-terminus located within the viral particle. The region immediately upstream of this protein exhibits a strong match to the TRS consensus (Table 2), indicating that a transcript
5 initiates from this site. The large number of cysteine residues (6) may result in cross linking of the amino acids. Amino acids ICTVVQRCASNKPHVLEDPCKVQH (SEQ ID NO: 192) of this protein may be secreted. The secreted amino acids exhibit homology to toxin proteins, for example, to the conotoxin of *Conus ventricosus* (Figure 27). Antigenic peptides from the hydrophilic (secreted) region, for example,
10 CICTVVQRCASNKPHVLEDPCK (SEQ ID NO: 193), were used to generate monoclonal antibodies using standard techniques. Furthermore, the C terminal amino acids form a sequence that shares homology to farnesylation sites (CKQH), which generally require C terminal location to be functional. This protein may act as a virulence factor and/or may facilitate transmission to humans.

15 ORF10 (Figure 2; nucleotides 27849-28100 of the 29,736-base genome sequence) or ORF11 (Figure 12; nucleotides 27,864-28118 of the 29,751-base genome sequence) encoding a protein of 84 amino acids (Figure 24; SEQ ID NO: 72) exhibited only very short (9-10 residues) matches to a region of the human coronavirus E2 glycoprotein precursor (starting at residue 801). Analysis by SignalP and TMHMM
20 predict a soluble protein. A detectable alignment to the TRS consensus sequence was also found (Table 2).

The protein (422 amino acids; Figure 8; SEQ ID NO: 36) encoded by the Nucleocapsid gene (Figure 2; nucleotides 28105-29370 of the 29,736-base genome sequence; Figure 12, nucleotides 28,120-29,388 of the 29,751-base genome sequence)
25 aligns well with nucleocapsid proteins from other representative coronaviruses (Figures 10A-B), although a short lysine rich region (KTFPPTPEPKKDKKKKTDEAQ; SEQ ID NO: 14) is unique to SARS. This region is suggestive of a nuclear localization signal. Since some coronaviruses are able to replicate in enucleated cells, the SARS virus nucleocapsid protein may have evolved a novel nuclear function, which may play a role
30 in pathogenesis. In addition, the basic nature of this peptide suggests it may assist in RNA binding. The SARS nucleocapsid protein is also a good candidate for diagnostic tests.

ORF 13 (Fig. 12; nucleotides 28,130 – 28,426 of the 29,751-base genome sequence) encodes a novel protein of 98 amino acids (Figure 25; SEQ ID NO: 73).
 ORF 14 (Fig. 12; nucleotides 28,583 – 28,795 of the 29,751-base genome sequence) encodes a novel protein of 70 amino acids (Figure 26; SEQ ID NO: 74). TMPred
 5 predicts a single transmembrane helix VVAVIQEIQLLAAVGEILLLEW (SEQ ID NO: 194).

Various features of the SARS virus genome are summarised in Table 3. While Table 3 refers to the 29,751-base genome sequence, the features are also applicable to the 29,736-base genome sequence (SEQ ID NOs: 1 and 2).

10

Table 3. Features of the SARS virus 29,751-base genome sequence.

Feature	Start – End ¹	No. amino acids	No. bases	Frame	TRS
Orf 1a	265 – 13,398	4,382	13,149	+1	N/A
Orf 1b	13,398 – 21,485	2,628	7,887	+3	N/A
S protein	21,492 – 25,259	1,255	3,768	+3	Strong
Orf 3	25,268 – 26,092	274	825	+2	Strong
Orf 4	25,689 – 26,153	154	465	+3	Absent ²
E protein	26,117 – 26,347	76	231	+2	Weak
M protein	26,398 – 27,063	221	666	+1	Strong
Orf 7	27,074 – 27,265	63	192	+2	Weak
Orf 8	27,273 – 27,641	122	369	+3	Strong
Orf 9	27,638 – 27,772	44	135	+2	Weak
Orf 10	27,779 – 27,898	39	120	+2	Strong
Orf 11	27,864 – 28,118	84	255	+3	Weak
N protein	28,120 – 29,388	422	1,269	+1	Strong
Orf 13 ³	28,130 – 28,426	98	297	+2	Absent ²
Orf 14 ³	28,583 – 28,795	70	213	+2	Absent
s2m motif	29,590 – 29,621	N/A	30	N/A	N/A

1. End coordinates include the stop codon, except for ORF 1a and s2m.

2 These ORFs overlap substantially or completely with other and may share TRSs.

15 N/A indicates not applicable.

Various polymorphisms may exist in the SARS virus. In the SARS 29,736-base genome sequences (SEQ ID NO: 1 or 2), for example, nucleotides 7904, 16607, 19168,

24857, or 26842 may be C or T; or nucleotides 19049, 23205, or 25283 may be G or A, and in the SARS 29,751-base genome sequence (SEQ ID NO: 15), for example, nucleotides 7919, 16622, 19183, 24872, or 26857 may be C or T; or nucleotides 19064, 23220, or 25298 may be G or A. In some embodiments, the nucleotide changes may result in no change in the encoded amino acid, or in a conservative or non-conservative change in the encoded amino acid. In some embodiments, a nucleotide change, as described herein, at position 7904 or 7919, may result in a A to V amino acid substitution, in the Replicase 1A protein coding region; a change at position 19168 or 19183 may result in a V to A amino acid substitution, in the Replicase IB protein coding region; a change at position 23205 or 23220 may result in a A to S amino acid substitution (non-conservative change), affecting the Spike glycoprotein coding region; a change at position 25283 or 25298 may result in a R to G amino acid substitution (non-conservative change), affecting ORF3; or a change at position 26842 or 26857 may result in a S to P amino acid substitution (non-conservative change), affecting the Nucleocapsid protein coding region, in the SARS 29,736-base (SEQ ID NO: 1 or 2) and 29,751-base genome (SEQ ID NO: 15) sequences, respectively. In various embodiments, a nucleotide or amino acid sequence including a particular polymorphism may be selected, for example, for use in the methods of the invention, or may be excluded, for example, from a particular use according to the invention.

Various alternative embodiments of the invention are described below. These embodiments include, without limitation, identification and use of SARS virus nucleic acid and amino acid sequences for diagnostic or therapeutic uses.

Diagnosis of SARS virus-related disorders

A SARS virus-related disorder is any disorder that is mediated by the SARS virus, or by a nucleic acid molecule or polypeptide derived from the SARS virus. Accordingly, SARS virus nucleic acid molecules and polypeptides may be used to diagnose and identify a SARS virus-related disorder in a mammal, for example, a human or a domestic, farm, wild, or experimental animal. In some embodiments, SARS virus nucleic acid molecules and polypeptides may be used to screen such animals, e.g., civet cats, for the presence of SARS virus. A SARS virus-related disorder may be a hepatic, enteric, respiratory, or neurological disorder, and may be

accompanied by one or more symptoms or indications including, but not limited to, fever, cough, shortness of breath, headache, low blood oxygen concentration, liver damage, or reduced lymphocyte numbers. Accordingly, samples for diagnosis may be obtained from cells, blood, serum, plasma, urine, stool, conjunctiva, sputum, asopharyngeal or oropharyngeal swabs, tracheal aspirates, bronchalveolar lavage, pleural fluid, amniotic fluid, or any other specimen, or any extract thereof, or by tissue biopsy of for example lungs or major organs, obtained from a patient (human or animal), test subject, or experimental animal.

A SARS virus-related disorder may be diagnosed by amplifying a SARS nucleic acid molecule or fragment thereof from a sample. Probes or primers for use in amplification may be prepared using standard techniques. In some embodiments, probes or primers are selected from regions of a SARS virus genome as described herein that show limited sequence homology or identity (e.g., less than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% identity) to other viruses or pathogens, or to host sequences.

Nucleic acid sequences can be amplified as needed by methods known in the art. For example, this can be accomplished by e.g., polymerase chain reaction "PCR" of DNA or of RNA by reverse transcriptase-PCR or "RT-PCR" (See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, Calif., 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. No. 4,683,202 issued July 28, 1987 to Mullis) Variations of standard PCR techniques, such as for example real time RT-PCR using internal as well as amplification primers, resulting in increased sensitivity and speed, and reduction of risk of sample contamination (see for example Higuchi, R., et al., "Kinetic PCR Analysis: Real-time Monitoring of DNA Amplification Reactions," Bio/Technology, vol. 11, pp. 1026-1030 (1993); Heid et al., "Real Time Quantitative PCT", Genome Research, 1996, pp. 986-994; Gibson UE et al., "A novel method for real time quantitative RT-PCR," Genome Res. 1996 Oct;6(10):995-1001), or the "Taqman" approach to PCR, described by for example Holland et al, Proc. Natl. Acad. Sci., 88: 7276-7280 (1991), may be performed.

Other suitable amplification and analytical methods include the single base primer extension (see for example U.S. Patent No. 6,004,744), mini-sequencing, ligase chain reaction (LCR) (see for example Wu and Wallace, Genomics 4, 560 (1989), Landegren et al., Science 241, 1077 (1988), transcription amplification (Kwoh et al.,
5 Proc. Natl. Acad. Sci. USA 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., Proc. Nat. Acad. Sci. USA, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification
10 products in a ratio of about 30 or 100 to 1, respectively.

A SARS virus-related disorder may also be diagnosed using an antibody directed against a SARS virus nucleic acid or amino acid sequence that specifically binds a nucleic acid molecule or polypeptide. In an alternative embodiment, the antibody may be directed against a SARS polypeptide, for example, the S polypeptide
15 or fragment thereof that is located on the surface of the SARS virion. Methods for preparation of antibodies or for assaying antibody binding are well known in the art.

Serological diagnosis may included detection of antibodies against a SARS virus polypeptide or nucleic acid molecule, e.g., the Nucleocapsid protein, produced in response to infection using techniques such as indirect fluorescent antibody testing or
20 enzyme-linked immunosorbent assays (ELISA). A SARS virus-related disorder may also be diagnosed by for example performing *in situ* probe hybridization studies on tissue specimens.

In some aspects, diagnostic tests as described herein or known to those of skill in the art may be performed for SARS virus variants that exhibit increased
25 pathogenicity, such as strains having redundant sequences.

In some embodiments, reagents for diagnosis (e.g. probes, primers, antibodies, etc.) may be provided in kits which may optionally include instructions for using the reagent or may include other reagents for performing the appropriate assay e.g., controls, standards, buffers, etc.

30
Therapy or Prophylaxis for SARS virus-related disorders

Compounds according to the invention may also be used to provide therapeutics or prophylactics for SARS virus-related disorders. Accordingly, such compounds may be used to treat a mammal, for example, a human or a domestic, farm, wild, or experimental animal that has or is at risk for a SARS virus-related disorder. Such compounds may include, without limitation, compounds that interfere with SARS virus replication, expression of SARS virus proteins, or the ability of the SARS virus to infect a host cell. Accordingly, in some embodiments, compounds that act as antagonists to SARS virus polypeptides may be used as therapeutics or prophylactics for SARS virus related disorders. In some embodiments, purified SARS virus polypeptides may be used as for example competitive inhibitors to disrupt viral function. For example, a Spike protein lacking a functional domain, or having some other modification that maintains binding but reduces or eliminates pathogenicity, may be used to disrupt viral function. In some embodiments, antibodies that bind SARS virus polypeptides or nucleic acid molecules, for example, humanized antibodies, may be used as therapeutics or prophylactics.

In some embodiments, the SARS-virus compounds may be used as vaccines, or may be used to develop vaccines. For example, peptides derived from portions of SARS-virus proteins or polypeptides located on the outside of the virion or cell surface may be useful for vaccines or for generation of therapeutic or prophylactic antibodies.

A “vaccine” is a composition that includes materials that elicit a desired immune response. A vaccine may select, activate or expand memory B and T cells of the immune system to, for example, enable the elimination of infectious agents, such as a SARS virus, or a component thereof. In some embodiments, a vaccine includes a suitable carrier, such as an adjuvant, which is an agent that acts in a non-specific manner to increase the immune response to a specific antigen, or to a group of antigens, enabling the reduction of the quantity of antigen in any given vaccine dose, or the reduction of the frequency of dosage required to generate the desired immune response.

Vaccines according to the invention may include SARS virus polypeptides and nucleic acid molecules described herein, or immunogenic fragments thereof. In some embodiments, a SARS virus Spike polypeptide, Envelope polypeptide, or membrane glycoprotein or fragments thereof may be suitable for vaccine applications. In some

embodiments, the vaccines may be multivalent and include one or more epitopes from a SARS virus polypeptide or fragment thereof.

In some embodiments of the invention, a vaccine may include a live or killed microorganism e.g., a SARS virus or a component thereof. If a live SARS virus is used, which may be administered in the form of an oral vaccine, is may contain non-revertible genetic alterations (for example, large deletions or insertions in the genomic sequence) that reduce or eliminate the virulence of the virus ("attenuated virus"), but not its induction of an immune response. In some embodiments, a live vaccine may include an attenuated non-SARS microorganism (e.g, bacteria or virus such as vaccinia virus) that is capable of expressing a SARS virus polypeptide or immunogenic fragment thereof as described herein. In some embodiments, a vaccine may include SARS virus polypeptides or nucleic acid molecules having modifications that facilitate ease of administration. For example, an indigestible SARS virus polypeptide or nucleic acid molecule may be used for oral administration, and a modification that is suitable for inhalation may be used for administration to the lung.

A "nucleic acid vaccine" or "DNA vaccine" as used herein, is a nucleic acid construct comprising a polynucleotide encoding a polypeptide antigen, particularly an antigenic amino acid subsequence identified by methods described herein or known in the art. The nucleic acid construct can also include transcriptional promoter elements, enhancer elements, splicing signals, termination and polyadenylation signals, and other nucleic acid sequences. Thus, a nucleic acid vaccine is generally introduced into a subject animal using for example one or more DNA plasmids including one or more antigen-coding sequences (for example, a SARS virus Envelope polypeptide or membrane glycoprotein sequence) that are capable of transfecting cells in vivo and inducing an immune response (see for example Whalen RG et al. DNA-mediated immunization and the energetic immune response to hepatitis B surface antigen. Clin Immunol Immunopathol 1995;75:1-12; Wolff JA et al. Direct gene transfer into mouse muscle in vivo. Science 1990;247:1465-8; Fynan EF et al. DNA vaccines: protective immunizations by parental, mucosal, and genegun inoculations. Proc Natl Acad Sci USA 1993; 90:11478-82). In some embodiments, a library of nucleic acid fragments may be prepared by cloning SARS virus genomic DNA into a plasmid expression vector using known techniques and the library then used as a nucleic acid vaccine (see

for example Barry MA, et al. Protection against mycoplasma infection using expression-library immunization. Nature 1995;377:632-5).

The subject is administered the nucleic acid vaccine using standard methods.

The vertebrate can be administered parenterally, subcutaneously, intravenously,
5 intraperitoneally, intradermally, intramuscularly, topically, orally, rectally, nasally,
buccally, vaginally, by inhalation spray, or via an implanted reservoir in dosage
formulations containing conventional non-toxic, physiologically acceptable carriers or
vehicles. Alternatively, the subject is administered the nucleic acid vaccine through the
use of a particle acceleration or bombardment instrument (a "gene gun"). The form in
10 which it is administered (e.g., capsule, tablet, solution, emulsion) will depend in part on
the route by which it is administered. For example, for mucosal administration, nose
drops, inhalants or suppositories can be used. The nucleic acid vaccine can be
administered in conjunction with known adjuvants. The adjuvant is administered in a
sufficient amount, which is that amount that is sufficient to generate an enhanced
15 immune response to the nucleic acid vaccine. The adjuvant can be administered prior to
(e.g., 1 or more days before) inoculation with the nucleic acid vaccine; concurrently
with (e.g., within 24 hours of) inoculation with the nucleic acid vaccine;
contemporaneously (simultaneously) with the nucleic acid vaccine (e.g., the adjuvant is
mixed with the nucleic acid vaccine, and the mixture is administered to the vertebrate);
20 or after (e.g., 1 or more days after) inoculation with the nucleic acid vaccine. The
adjuvant can also be administered at more than one time (e.g., prior to inoculation with
the nucleic acid vaccine and also after inoculation with the nucleic acid vaccine). As
used herein, the term "in conjunction with" encompasses any time period, including
those specifically described herein and combinations of the time periods specifically
25 described herein, during which the adjuvant can be administered so as to generate an
enhanced immune response to the nucleic acid vaccine (e.g., an increased antibody titer
to the antigen encoded by the nucleic acid vaccine, or an increased antibody titer to the
pathogenic agent). The adjuvant and the nucleic acid vaccine can be administered at
approximately the same location on the vertebrate; for example, both the adjuvant and
30 the nucleic acid vaccine are administered at a marked site on a limb of the subject.

In some embodiments, expression of a SARS virus gene or coding or non-
coding region of interest may be inhibited or prevented using RNA interference (RNAi)

technology, a type of post-transcriptional gene silencing. RNAi may be used to create a functional “knockout”, i.e. a system in which the expression of a gene or coding or non-coding region of interest is reduced, resulting in an overall reduction of the encoded product. As such, RNAi may be performed to target a nucleic acid of interest or

5 fragment or variant thereof, to in turn reduce its expression and the level of activity of the product which it encodes. Such a system may be used for therapy or prophylaxis, as well as for functional studies. RNAi is described in for example published US patent applications 20020173478 (Gewirtz; published November 21, 2002) and 20020132788 (Lewis *et al.*; published November 7, 2002). Reagents and kits for performing RNAi
10 are available commercially from for example Ambion Inc. (Austin, TX, USA) and New England Biolabs Inc. (Beverly, MA, USA).

The initial agent for RNAi in some systems is thought to be dsRNA molecule corresponding to a target nucleic acid. The dsRNA is then thought to be cleaved into short interfering RNAs (siRNAs) which are 21-23 nucleotides in length (19-21 bp
15 duplexes, each with 2 nucleotide 3' overhangs). The enzyme thought to effect this first cleavage step has been referred to as “Dicer” and is categorized as a member of the Rnase III family of dsRNA-specific ribonucleases. Alternatively, RNAi may be effected via directly introducing into the cell, or generating within the cell by introducing into the cell a suitable precursor (e.g. vector, etc.) of such an siRNA or
20 siRNA-like molecule. An siRNA may then associate with other intracellular components to form an RNA-induced silencing complex (RISC). The RISC thus formed may subsequently target a transcript of interest via base-pairing interactions between its siRNA component and the target transcript by virtue of homology, resulting in the cleavage of the target transcript approximately 12 nucleotides from the 3' end of
25 the siRNA. Thus the target mRNA is cleaved and the level of protein product it encodes is reduced.

RNAi may be effected by the introduction of suitable *in vitro* synthesized siRNA or siRNA-like molecules into cells. RNAi may for example be performed using chemically-synthesized RNA, for which suitable RNA molecules may chemically
30 synthesized using known methods. Alternatively, suitable expression vectors may be used to transcribe such RNA either *in vitro* or *in vivo*. *In vitro* transcription of sense and antisense strands (encoded by sequences present on the same vector or on separate

vectors) may be effected using for example T7 RNA polymerase, in which case the vector may comprise a suitable coding sequence operably-linked to a T7 promoter. The *in vitro*-transcribed RNA may in embodiments be processed (e.g. using *E. coli* RNase III) *in vitro* to a size conducive to RNAi. The sense and antisense transcripts combined to form an RNA duplex which is introduced into a target cell of interest. Other vectors may be used, which express small hairpin RNAs (shRNAs) which can be processed into siRNA-like molecules. Various vector-based methods are known in the art. Various methods for introducing such vectors into cells, either *in vitro* or *in vivo* (e.g. gene therapy) are known in the art.

Accordingly, in an embodiment, expression of a polypeptide including an amino acid sequence substantially identical to a SARS virus sequence may be inhibited by introducing into or generating within a cell an siRNA or siRNA-like molecule corresponding to a nucleic acid molecule encoding the polypeptide or fragment thereof, or to an nucleic acid homologous thereto. In various embodiments such a method may entail the direct administration of the siRNA or siRNA-like molecule into a cell, or use of the vector-based methods described above. In an embodiment, the siRNA or siRNA-like molecule is less than about 30 nucleotides in length. In a further embodiment, the siRNA or siRNA-like molecules are about 21-23 nucleotides in length. In an embodiment, siRNA or siRNA-like molecules comprise and 19-21 bp duplex portion, each strand having a 2 nucleotide 3' overhang. In embodiments, the siRNA or siRNA-like molecule is substantially identical to a nucleic acid encoding the polypeptide or a fragment or variant (or a fragment of a variant) thereof. Such a variant is capable of encoding a protein having the activity of a SARS virus polypeptide. In embodiments, the sense strand of the siRNA or siRNA-like molecule is substantially identical to a SARS virus nucleic acid molecule or a fragment thereof (RNA having U in place of T residues of the DNA sequence).

SARS Virus Protein Expression

In general, SARS virus polypeptides according to the invention, may be produced by transformation of a suitable host cell with all or part of a SARS virus polypeptide-encoding genomic or cDNA molecule or fragment thereof (e.g., the genomic DNA or cDNAs described herein) in a suitable expression vehicle. Those

skilled in the field of molecular biology will understand that any of a wide variety of expression systems may be used to provide the recombinant protein. The precise host cell used is not critical to the invention. The SARS virus polypeptide may be produced in a prokaryotic host (e.g., *E. coli* or a virus, for example, a coronavirus such as human OC43 or 229E, a bovine coronavirus, or a virus used for gene therapy, such as an adenovirus) or in a eukaryotic host (e.g., *Saccharomyces cerevisiae*, insect cells, e.g., Sf21 cells, or mammalian cells, e.g., COS 1, NIH 3T3, VeroE6, or HeLa cells). Such cells are available from a wide range of sources (e.g., the American Type Culture Collection, Rockland, Md.; also, see, e.g., Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1994). The method of transformation or transfection and the choice of expression vehicle will depend on the host system selected. Transformation and transfection methods are described, e.g., in Ausubel et al. (*supra*); expression vehicles may be chosen from those provided, e.g., in *Cloning Vectors: A Laboratory Manual*, P. H. Pouwels et al, 1985, Supp. 1987), or from commercially available sources. Suitable animal models, e.g. a ferret animal model, or any other animal model suitable for analysis of SARS virus infection or expression of SARS virus nucleic acid molecules may be used.

In an alternative embodiment, the baculovirus expression system (using, for example, the vector pBacPAK9) available from Clontech (Pal Alto, Calif.) may be used. If desired, this system may be used in conjunction with other protein expression techniques, for example, the myc tag approach described by Evan et al. (*Mol. Cell Biol.* 5:3610-3616, 1985). In an alternative embodiment, a SARS virus polypeptide may be produced by a stably-transfected mammalian cell line. A number of vectors suitable for stable transfection of mammalian cells are available to the public, e.g., see Pouwels et al (*supra*); methods for constructing such cell lines are also publicly available, e.g., in Ausubel et al. (*supra*). In one example, cDNA encoding the SARS virus polypeptide is cloned into an expression vector which includes the dihydrofolate reductase (DHFR) gene. Integration of the plasmid and, therefore, the SARS virus polypeptide-encoding gene into the host cell chromosome is selected for by inclusion of 0.01-300 μ M methotrexate in the cell culture medium (as described in Ausubel et al., *supra*). This dominant selection can be accomplished in most cell types. Recombinant protein expression can be increased by DHFR-mediated amplification of the transfected gene.

Methods for selecting cell lines bearing gene amplifications are described in Ausubel et al. (supra); such methods generally involve extended culture in medium containing gradually increasing levels of methotrexate. DHFR-containing expression vectors commonly used for this purpose include pCVSEII-DHFR and pAdD26SV(A) (described in Ausubel et al., supra). Any of the host cells described above or, preferably, a DHFR-deficient CHO cell line (e.g., CHO DHFR.sup.- cells, ATCC Accession No. CRL 9096) are among the host cells preferred for DHFR selection of a stably-transfected cell line or DHFR-mediated gene amplification.

Once the recombinant SARS virus polypeptide is expressed, it is isolated, e.g., using affinity chromatography. In one example, an anti-SARS virus polypeptide antibody (e.g., produced as described herein) may be attached to a column and used to isolate the SARS virus polypeptide. Lysis and fractionation of SARS virus polypeptide-harboring cells prior to affinity chromatography may be performed by standard methods (see, e.g., Ausubel et al., supra). In another example, SARS virus polypeptides may be purified or substantially purified from a mixture of compounds such as an extract or supernatant obtained from cells (Ausubel et al., supra). Standard purification techniques can be used to progressively eliminate undesirable compounds from the mixture until a single compound or minimal number of effective compounds has been isolated.

Once isolated, the recombinant protein can, if desired, be further purified, e.g., by high performance liquid chromatography (see, e.g., Fisher, Laboratory Techniques In Biochemistry And Molecular Biology, eds., Work and Burdon, Elsevier, 1980).

Polypeptides of the invention, particularly short SARS virus peptide fragments, can also be produced by chemical synthesis (e.g., by the methods described in Solid Phase Peptide Synthesis, 2nd ed., 1984 The Pierce Chemical Co., Rockford, Ill.).

These general techniques of polypeptide expression and purification can also be used to produce and isolate useful SARSvirus protein fragments or analogs (described herein).

In certain alternative embodiments, the SARS polypeptide might have attached any one of a variety of tags. Tags can be amino acid tags or chemical tags and can be added for the purpose of purification (for example a 6-histidine tag for purification over a nickel column). In other preferred embodiments, various labels can be used as means

for detecting binding of a SARS polypeptide to another polypeptide, for example to a cell surface receptor. Alternatively, SARS DNA or RNA may be labeled for detection, for example in a hybridization assay. SARS virus nucleic acids or proteins, or derivatives thereof, may be directly or indirectly labeled, for example, with a
5 radioscope, a fluorescent compound, a bioluminescent compound, a chemiluminescent compound, a metal chelator or an enzyme. Those of ordinary skill in the art will know of other suitable labels or will be able to ascertain such, using routine experimentation. In yet another embodiment of the invention, the polypeptides disclosed herein, or derivatives thereof, are linked to toxins.

Isolation and Identification of Additional SARS virus molecules

Based on the SARS virus sequences described herein, the isolation and identification of additional SARS virus-related sequences such as SARS virus genes and of additional SARS virus strains or isolates is made possible using standard
15 techniques. In addition, the SARS virus sequences provided herein also provide the basis for identification of homologous sequences from other species and genera from both prokaryotes and eukaryotes such as viruses, bacteria, fungi, parasites, yeast, and/or mammals. In some embodiments, the nucleic acid sequences described herein may be used to design probes or primers, including degenerate oligonucleotide probes or
20 primers, based upon the sequence of either DNA strand. The probes or primers may then be used to screen genomic or cDNA libraries for sequences from for example naturally occurring variants or isolates of SARS viruses, using standard amplification or hybridization techniques.

In some embodiments, binding partners may be identified by tagging the
25 polypeptides of the invention (e.g., those substantially identical to SARS virus polypeptides described herein) with an epitope sequence (e.g., FLAG or 2HA), and delivering it into host cells, either by transfection with a suitable vector containing a nucleic acid sequence encoding a polypeptide of the invention, followed by immunoprecipitation and identification of the binding partner. Cells may be infected
30 with strains expressing the FLAG or 2HA fusions, followed by lysis and immunoprecipitation with anti-FLAG or anti-2HA antibodies. Binding partners may be identified by mass spectroscopy. If the polypeptide of the invention is not produced in

sufficient quantities, such a method may not deliver enough tagged protein to identify its partner. As part of a complementary approach, each polypeptide of the invention may be cloned into a mammalian transfection vector fused to, for example, 2HA, GFP and/or FLAG. Following transfection, HeLa cells may be lysed and the tagged
5 polypeptide immunoprecipitated. The binding partner may be identified by SDS PAGE followed by mass spectroscopy.

In some embodiments, polypeptides or antibodies of the invention may be tagged, produced, and used for example on affinity columns and/or immunological assays to identify and/or confirm identified target compounds. FLAG, HA, and/or His
10 tagged proteins can be used for such affinity columns to pull out host cell factors from cell extracts, and any hits may be validated by standard binding assays, saturation curves, and other methods as described herein or known to those of skill in the art.

In some embodiments, a two hybrid system may be used to study protein-protein interactions. The nucleic acid sequences described herein, or sequences
15 substantially identical thereto, can be cloned into the pBT bait plasmid of the two hybrid system, and a commercially available murine spleen library of 5×10^6 independent clones, may be used as the target library for the baits. Potential hits may be further characterized by recovering the plasmids and retransforming to reduce false positives resulting from clonal bait variants and library target clones which activate the
20 reporter genes independent of the cloned bait. Reproducible hits may be studied further as described herein.

Virulence may be assayed as described herein or as known to those of skill in the art. Once coding sequences have been identified, they may be isolated using standard cloning techniques, and inserted into any suitable vector or replicon for, for example,
25 production of polypeptides. Such vectors and replicons include, without limitation, bacteriophage X (E. coli), pBR322 (E. coli), pACYC177 (E. coli), pKT230 (gram-negative bacteria), pGV1 106 (gram-negative bacteria), pLAFRI (gram-negative bacteria), pME290 (non-E. coli gram-negative bacteria), pHV14 (E. coli and Bacillus subtilis), pBD9 (Bacillus), pIJ61 (Streptomyces), pUC6 (Streptomyces), YIp5
30 (Saccharomyces), YCpl9 (Saccharomyces) or bovine papilloma virus (mammalian cells). In general, the polypeptides of the invention may be produced in any suitable host cell transformed or transfected with a suitable vector. The method of

transformation or transfection and the choice of expression vehicle will depend on the host system selected. A wide variety of expression systems may be used, and the precise host cell used is not critical to the invention. For example, a polypeptide according to the invention may be produced in a prokaryotic host (e.g., *E. coli*) or in a eukaryotic host (e.g., *Saccharomyces cerevisiae*, insect cells, e.g., Sf21 cells, or mammalian cells, e.g., NIH 3T3, HeLa, or COS cells). Such cells are available from a wide range of sources (e.g., the American Type Culture Collection, Manassus, VA.). Bacterial expression systems for polypeptide production include the *E. coli* pET expression system (Novagen, Inc., Madison, Wis.), and the pGEX expression system (Pharmacia).

Compounds

In one aspect, compounds according to the invention include SARS virus nucleic acid molecules and polypeptides, such as the sequences disclosed in the Figures and Tables herein, and throughout the specification, and fragments thereof. In alternative embodiments, compounds according to the invention may be nucleic acid molecules that are at least 10 nucleotides in length, and that are derived from the sequences described herein. In alternative embodiments, compounds according to the invention may be peptides that are at least 5 amino acids in length, and that are derived from the sequences described herein.

In alternative embodiments, a compound according to the invention can be a non-peptide molecule as well as a peptide or peptide analogue. A peptide or peptide analogue will generally be as small as feasible while retaining full biological activity. A non-peptide molecule can be any molecule that exhibits biological activity as described herein or known in the art. Biological activity can, for example, be measured in terms of ability to elicit a cytotoxic response, to mediate DNA replication, or any other function of a SARS virus molecule.

Compounds can be prepared by, for example, replacing, deleting, or inserting an amino acid residue of SARS peptide or peptide analogue, as described herein, with other conservative amino acid residues, i.e., residues having similar physical, biological, or chemical properties, and screening for biological function.

It is well known in the art that some modifications and changes can be made in the structure of a polypeptide without substantially altering the biological function of that peptide, to obtain a biologically equivalent polypeptide. Such modifications may be made for the purpose of modifying function, or for facilitating administration or enhancing stability or inhibiting breakdown for, for example, therapeutic uses. For example, an indigestible SARS virus compound according to the invention may be used for oral administration; a modification that is suitable for inhalation may be used for administration to the lung; or addition of a leader sequence may increase protein expression levels.

In one aspect of the invention, SARS virus-derived peptides or epitopes may include peptides that differ from a portion of a native leader, protein or SARS virus sequence by conservative amino acid substitutions. The peptides and epitopes of the present invention also extend to biologically equivalent peptides that differ from a portion of the sequence of novel peptides of the present invention by conservative amino acid substitutions. As used herein, the term "conserved amino acid substitutions" refers to the substitution of one amino acid for another at a given location in the peptide, where the substitution can be made without substantial loss of the relevant function. In making such changes, substitutions of like amino acid residues can be made on the basis of relative similarity of side-chain substituents, for example, their size, charge, hydrophobicity, hydrophilicity, and the like, and such substitutions may be assayed for their effect on the function of the peptide by routine testing.

In some embodiments, conserved amino acid substitutions may be made where an amino acid residue is substituted for another having a similar hydrophilicity value (e.g., within a value of plus or minus 2.0), where the following may be an amino acid having a hydropathic index of about -1.6 such as Tyr (-1.3) or Pro (-1.6)s are assigned to amino acid residues (as detailed in United States Patent No. 4,554,101, incorporated herein by reference): Arg (+3.0); Lys (+3.0); Asp (+3.0); Glu (+3.0); Ser (+0.3); Asn (+0.2); Gln (+0.2); Gly (0); Pro (-0.5); Thr (-0.4); Ala (-0.5); His (-0.5); Cys (-1.0); Met (-1.3); Val (-1.5); Leu (-1.8); Ile (-1.8); Tyr (-2.3); Phe (-2.5); and Trp (-3.4).

In alternative embodiments, conserved amino acid substitutions may be made where an amino acid residue is substituted for another having a similar hydropathic index (e.g., within a value of plus or minus 2.0). In such embodiments, each amino acid

residue may be assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics, as follows: Ile (+4.5); Val (+4.2); Leu (+3.8); Phe (+2.8); Cys (+2.5); Met (+1.9); Ala (+1.8); Gly (-0.4); Thr (-0.7); Ser (-0.8); Trp (-0.9); Tyr (-1.3); Pro (-1.6); His (-3.2); Glu (-3.5); Gln (-3.5); Asp (-3.5); Asn (-3.5); Lys (-3.9); and Arg (-4.5).

In alternative embodiments, conserved amino acid substitutions may be made where an amino acid residue is substituted for another in the same class, where the amino acids are divided into non-polar, acidic, basic and neutral classes, as follows: non-polar: Ala, Val, Leu, Ile, Phe, Trp, Pro, Met; acidic: Asp, Glu; basic: Lys, Arg, His; neutral: Gly, Ser, Thr, Cys, Asn, Gln, Tyr.

Conservative amino acid changes can include the substitution of an L-amino acid by the corresponding D-amino acid, by a conservative D-amino acid, or by a naturally-occurring, non-genetically encoded form of amino acid, as well as a conservative substitution of an L-amino acid. Naturally-occurring non-genetically encoded amino acids include beta-alanine, 3-amino-propionic acid, 2,3-diamino propionic acid, alpha-aminoisobutyric acid, 4-amino-butyric acid, N-methylglycine (sarcosine), hydroxyproline, ornithine, citrulline, t-butylalanine, t-butylglycine, N-methylisoleucine, phenylglycine, cyclohexylalanine, norleucine, norvaline, 2-naphthylalanine, pyridylalanine, 3-benzothienyl alanine, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, penicillamine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, beta-2-thienylalanine, methionine sulfoxide, homoarginine, N-acetyl lysine, 2-amino butyric acid, 2-amino butyric acid, 2,4,-diamino butyric acid, p-aminophenylalanine, N-methylvaline, homocysteine, homoserine, cysteic acid, epsilon-amino hexanoic acid, delta-amino valeric acid, or 2,3-diaminobutyric acid.

In alternative embodiments, conservative amino acid changes include changes based on considerations of hydrophilicity or hydrophobicity, size or volume, or charge. Amino acids can be generally characterized as hydrophobic or hydrophilic, depending primarily on the properties of the amino acid side chain. A hydrophobic amino acid exhibits a hydrophobicity of greater than zero, and a hydrophilic amino acid exhibits a hydrophilicity of less than zero, based on the normalized consensus hydrophobicity scale of Eisenberg *et al.* (*J. Mol. Bio.* 179:125-142, 184). Genetically encoded

hydrophobic amino acids include Gly, Ala, Phe, Val, Leu, Ile, Pro, Met and Trp, and genetically encoded hydrophilic amino acids include Thr, His, Glu, Gln, Asp, Arg, Ser, and Lys. Non-genetically encoded hydrophobic amino acids include t-butylalanine, while non-genetically encoded hydrophilic amino acids include citrulline and

5 homocysteine.

Hydrophobic or hydrophilic amino acids can be further subdivided based on the characteristics of their side chains. For example, an aromatic amino acid is a hydrophobic amino acid with a side chain containing at least one aromatic or heteroaromatic ring, which may contain one or more substituents such as -OH, -SH, -
10 CN, -F, -Cl, -Br, -I, -NO₂, -NO, -NH₂, -NHR, -NRR, -C(O)R, -C(O)OH, -C(O)OR, -C(O)NH₂, -C(O)NHR, -C(O)NRR, etc., where R is independently (C₁-C₆) alkyl, substituted (C₁-C₆) alkyl, (C₁-C₆) alkenyl, substituted (C₁-C₆) alkenyl, (C₁-C₆) alkynyl, substituted (C₁-C₆) alkynyl, (C₅-C₂₀) aryl, substituted (C₅-C₂₀) aryl, (C₆-C₂₆) alkaryl, substituted (C₆-C₂₆) alkaryl, 5-20 membered heteroaryl, substituted 5-20
15 membered heteroaryl, 6-26 membered alkheteroaryl or substituted 6-26 membered alkheteroaryl. Genetically encoded aromatic amino acids include Phe, Tyr, and Trp, while non-genetically encoded aromatic amino acids include phenylglycine, 2-naphthylalanine, beta-2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, and 4-
20 fluorophenylalanine.

An apolar amino acid is a hydrophobic amino acid with a side chain that is uncharged at physiological pH and which has bonds in which a pair of electrons shared in common by two atoms is generally held equally by each of the two atoms (i.e., the side chain is not polar). Genetically encoded apolar amino acids include Gly, Leu, Val,
25 Ile, Ala, and Met, while non-genetically encoded apolar amino acids include cyclohexylalanine. Apolar amino acids can be further subdivided to include aliphatic amino acids, which is a hydrophobic amino acid having an aliphatic hydrocarbon side chain. Genetically encoded aliphatic amino acids include Ala, Leu, Val, and Ile, while non-genetically encoded aliphatic amino acids include norleucine.

30 A polar amino acid is a hydrophilic amino acid with a side chain that is uncharged at physiological pH, but which has one bond in which the pair of electrons shared in common by two atoms is held more closely by one of the atoms. Genetically

encoded polar amino acids include Ser, Thr, Asn, and Gln, while non-genetically encoded polar amino acids include citrulline, N-acetyl lysine, and methionine sulfoxide.

5 An acidic amino acid is a hydrophilic amino acid with a side chain pKa value of less than 7. Acidic amino acids typically have negatively charged side chains at physiological pH due to loss of a hydrogen ion. Genetically encoded acidic amino acids include Asp and Glu. A basic amino acid is a hydrophilic amino acid with a side chain pKa value of greater than 7. Basic amino acids typically have positively charged side chains at physiological pH due to association with hydronium ion. Genetically
10 encoded basic amino acids include Arg, Lys, and His, while non-genetically encoded basic amino acids include the non-cyclic amino acids ornithine, 2,3,-diaminopropionic acid, 2,4-diaminobutyric acid, and homoarginine.

It will be appreciated by one skilled in the art that the above classifications are not absolute and that an amino acid may be classified in more than one category. In
15 addition, amino acids can be classified based on known behaviour and or characteristic chemical, physical, or biological properties based on specified assays or as compared with previously identified amino acids. Amino acids can also include bifunctional moieties having amino acid-like side chains.

Conservative changes can also include the substitution of a chemically
20 derivatised moiety for a non-derivatised residue, by for example, reaction of a functional side group of an amino acid. Thus, these substitutions can include compounds whose free amino groups have been derivatised to amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Similarly, free carboxyl groups can be derivatized to form
25 salts, methyl and ethyl esters or other types of esters or hydrazides, and side chains can be derivatized to form O-acyl or O-alkyl derivatives for free hydroxyl groups or N-im-benzylhistidine for the imidazole nitrogen of histidine. Peptide analogues also include amino acids that have been chemically altered, for example, by methylation, by amidation of the C-terminal amino acid by an alkylamine such as ethylamine,
30 ethanolamine, or ethylene diamine, or acylation or methylation of an amino acid side chain (such as acylation of the epsilon amino group of lysine). Peptide analogues can also include replacement of the amide linkage in the peptide with a substituted amide

(for example, groups of the formula $-C(O)-NR$, where R is (C_1-C_6) alkyl, (C_1-C_6) alkenyl, (C_1-C_6) alkynyl, substituted (C_1-C_6) alkyl, substituted (C_1-C_6) alkenyl, or substituted (C_1-C_6) alkynyl) or isostere of an amide linkage (for example, $-CH_2NH-$, $-CH_2S-$, $-CH_2CH_2-$, $-CH=CH-$ (cis and trans), $-C(O)CH_2-$, $-CH(OH)CH_2-$, or $-CH_2SO-$).

5 The compound can be covalently linked, for example, by polymerisation or conjugation, to form homopolymers or heteropolymers. Spacers and linkers, typically composed of small neutral molecules, such as amino acids that are uncharged under physiological conditions, can be used. Linkages can be achieved in a number of ways. For example, cysteine residues can be added at the peptide termini, and multiple
10 peptides can be covalently bonded by controlled oxidation. Alternatively, heterobifunctional agents, such as disulfide/amide forming agents or thioether/amide forming agents can be used. The compound can also be constrained, for example, by having cyclic portions.

In some embodiments, three dimensional molecular modeling techniques may
15 be used to identify or generate compounds that may be useful as therapeutics or diagnostics. Standard molecular modeling tools may be used, for example, those described in L-H Hung and R. Samudrala, PROTINFO: secondary and tertiary protein structure prediction, *Nucleic Acids Research*, 2003, Vol. 31, No. 13 3296-3299; A. Yamaguchi, et al., Enlarged FAMSBASE: protein 3D structure models of genome
20 sequences for 41 species, *Nucleic Acids Research*, 2003, Vol. 31, No. 1 463-468; J. Chen, et al., MMDB: Entrez's 3D-structure database, *Nucleic Acids Research*, 2003, Vol. 31, No. 1 474-477; R. A. Chiang, et al., The Structure Superposition Database, *Nucleic Acids Research*, 2003, Vol. 31, No. 1 505-510.

Peptides or peptide analogues can be synthesized by standard chemical
25 techniques, for example, by automated synthesis using solution or solid phase synthesis methodology. Automated peptide synthesizers are commercially available and use techniques well known in the art. Peptides and peptide analogues can also be prepared using recombinant DNA technology using standard methods such as those described in, for example, Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd ed.,
30 Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) or Ausubel *et al.* (*Current Protocols in Molecular Biology*, John Wiley & Sons, 1994).

Compounds, such as peptides (or analogues thereof) can be identified by routine experimentation by, for example, modifying residues within SARS peptides; introducing single or multiple amino acid substitutions, deletions, or insertions, and identifying those compounds that retain biological activity, *e.g.*, those compounds that have cytotoxic ability.

In general, candidate compounds for prevention or treatment of SARS virus-mediated disorders are identified from large libraries of both natural product or synthetic (or semi-synthetic) extracts or chemical libraries according to methods known in the art. Candidate or test compounds may include, without limitation, peptides, polypeptides, synthesised organic molecules, naturally occurring organic molecules, and nucleic acid molecules. In some embodiments, such compounds screen for the ability to inhibit SARS virus replication or pathogenicity, while maintaining the infected cell's ability to grow or survive.

Those skilled in the field of drug discovery and development will understand that the precise source of test extracts or compounds is not critical to the method(s) of the invention. Accordingly, virtually any number of chemical extracts or compounds can be screened using the exemplary methods described herein or using standard methods. Examples of such extracts or compounds include, but are not limited to, plant-, fungal-, prokaryotic- or animal-based extracts, fermentation broths, and synthetic compounds, as well as modification of existing compounds. Numerous methods are also available for generating random or directed synthesis (*e.g.*, semi-synthesis or total synthesis) of any number of chemical compounds, including, but not limited to, saccharide-, lipid-, peptide-, and nucleic acid-based compounds. Synthetic compound libraries are commercially available. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant, and animal extracts are commercially available from a number of sources, including Biotics (Sussex, UK), Xenova (Slough, UK), Harbor Branch Oceanographic Institute (Ft. Pierce, Fla.), and PharmaMar, U.S.A. (Cambridge, Mass.). In addition, natural and synthetically produced libraries of, for example, SARS virus polypeptides containing leader sequences, are produced, if desired, according to methods known in the art, *e.g.*, by standard extraction and fractionation methods. Furthermore, if desired, any library or compound is readily modified using standard chemical, physical, or biochemical methods.

When a crude extract is found to modulate cytotoxicity or viral infection, further fractionation of the positive lead extract is necessary to isolate chemical constituents responsible for the observed effect. Thus, the goal of the extraction, fractionation, and purification process is the careful characterization and identification of a chemical entity within the crude extract having, for example, anti-cytotoxicity or anti-viral properties. The same assays described herein for the detection of activities in mixtures of compounds can be used to purify the active component and to test derivatives thereof. Methods of fractionation and purification of such heterogenous extracts are known in the art. If desired, compounds shown to be useful agents for treatment are chemically modified according to methods known in the art. Compounds identified as being of therapeutic, prophylactic, diagnostic, or other value in for example cell culture systems, such as a Vero E6 culture system, may be subsequently analyzed using a ferret animal model, or any other animal model suitable for analysis of SARS.

Antibodies

The compounds of the invention can be used to prepare antibodies to SARS virus peptides, protein, polyproteins, or analogs thereof, or to SARS virus nucleic acid molecules or analogs thereof using standard techniques of preparation as, for example, described in Harlow and Lane (Antibodies; A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1988), or known to those skilled in the art. Antibodies may include polyclonal antibodies, monoclonal antibodies, hybrid antibodies (e.g., divalent antibodies having different pairs of heavy and light chains), chimeric antibodies (e.g., antibodies having constant and variable domains from different species and/or class), modified antibodies (e.g, antibodies in which the naturally occurring sequence has been altered by for example recombinant techniques), Fab antibodies, anti-idiotypic antibodies, etc. Antibodies can be tailored to minimise adverse host immune response by, for example, using chimeric antibodies containing an antigen binding domain from one species and the Fc portion from another species, or by using antibodies made from hybridomas of the appropriate species. For example, "humanized" antibodies may be used for administration to humans.

To generate SARS virus polypeptide-specific antibodies, a SARS virus polypeptide coding sequence may be expressed, for example, as a C-terminal fusion with glutathione S-transferase (GST) (Smith et al., Gene 67:31-40, 1988). The fusion polypeptide may then be purified on glutathione-Sepharose beads, eluted with
5 glutathione cleaved with thrombin (at the engineered cleavage site), and purified to the degree necessary for immunization of rabbits. Primary immunizations are carried out with Freud's complete adjuvant and subsequent immunizations with Freud's incomplete adjuvant. Antibody titres are monitored by Western blot and immunoprecipitation analyzes using the thrombin-cleaved SARS virus polypeptide fragment of the GST-
10 SARS virus fusion polypeptide. Immune sera are affinity purified using CNBr-Sepharose-coupled SARS virus polypeptide. Antiserum specificity is determined using a panel of unrelated GST polypeptides.

As an alternate or adjunct immunogen to GST fusion polypeptides, peptides corresponding to relatively unique hydrophilic SARS virus polypeptides may be
15 generated and coupled to keyhole limpet hemocyanin (KLH) through an introduced C-terminal lysine. Antiserum to each of these peptides is similarly affinity purified on peptides conjugated to BSA, and specificity tested in ELISA and Western blots using peptide conjugates, and by Western blot and immunoprecipitation using SARS virus polypeptide expressed as a GST fusion polypeptide.

20 Alternatively, monoclonal antibodies may be prepared using the SARS virus polypeptides described above and standard hybridoma technology (see, e.g., Kohler et al., Nature, 256:495, 1975; Kohler et al., Eur. J Immunol. 6:511, 1976; Kohler et al., Eur. J. Immunol. 6:292, 1976; Hammerling et al., In Monoclonal Antibodies and T Cell Hybridomas, Elsevier, NY, 1981; Ausubel et al., supra). Once produced, monoclonal
25 antibodies are also tested for specific SARS virus polypeptide recognition by Western blot or immunoprecipitation analysis (by the methods described in Ausubel et al., supra). Antibodies which specifically recognize SARS virus polypeptides are considered to be useful in the invention; such antibodies may be used, e.g., in an immunoassay to monitor the level of SARS virus polypeptides produced by a mammal
30 (for example, to determine the amount or location of a SARS virus polypeptide).

In an alternative embodiment, antibodies of the invention are not only produced using the whole SARS virus polypeptide, but using fragments of the SARS virus

polypeptide which are unique or which lie outside highly conserved regions and appear likely to be antigenic, by criteria such as high frequency of charged residues may also be used. In one specific example, such fragments are generated by standard techniques of PCR and cloned into the pGEX expression vector (Ausubel et al., supra). Fusion
5 polypeptides are expressed in *E. coli* and purified using a glutathione agarose affinity matrix as described in Ausubel et al. (supra). To attempt to minimize the potential problems of low affinity or specificity of antisera, two or three such fusions are generated for each polypeptide, and each fusion is injected into at least two rabbits. Antisera are raised by injections in a series, preferably including at least three booster
10 injections. SARS virus antibodies may also be prepared against SARS virus nucleic acid molecules.

Antibodies may be used as diagnostics, therapeutics, or prophylactics for SARS virus-related disorders. Antibodies may also be used to isolate SARS virus and compounds by for example affinity chromatography, or to identify SARS virus
15 compounds isolated or generated by other techniques.

Arrays and Libraries

In some aspects, biological assays, such as diagnostic or other assays, using high density nucleic acid, polypeptide, or antibody arrays, for example high density
20 miniaturized arrays or "microarrays," of SARS virus nucleic acid molecules or polypeptides, or antibodies capable of specifically binding such nucleic acid molecules or polypeptides, may be performed. Macroarrays, performed for example by manual spotting techniques, may also be used. Arrays generally require a solid support (for example, nylon, glass, ceramic, plastic, silicon, nitrocellulose or PVDF membranes,
25 microwells, microbeads, e.g., magnetic microbeads, etc.) to which the nucleic acid molecules or polypeptides or antibodies are attached in a specified two-dimensional arrangement, such that the pattern of hybridization is easily determinable. Suspension arrays (particles in suspension) that are coded to facilitate identification may also be used. SARS virus nucleic acid molecules or polypeptide
30 probes or targets may be compounds as described herein.

In some embodiments, high density nucleic acid arrays may for example be used to monitor the presence or level of expression of a large number of SARS virus

nucleic acid molecules or genes or for detecting or identifying SARS virus nucleic acid sequence variations, mutations or polymorphisms. For the purpose of such arrays, “nucleic acids” may include any polymer or oligomer of nucleosides or nucleotides (polynucleotides or oligonucleotides), which include pyrimidine and purine bases, preferably cytosine, thymine, and uracil, and adenine and guanine, respectively, or may include peptide nucleic acids (PNA). In an alternative aspect, the invention provides nucleic acid microarrays including a number of distinct nucleic acid sequence arrays of the invention, thus providing specific “sets” of sequences. The number of distinct sequences may for example be any integer between 2 and 1×10^5 , such as at least 10^2 , 10^3 , 10^4 , or 10^5 .

The invention also provides gene knockout and expression libraries. Thus, nucleic acid molecules encoding SARS virus polypeptides or proteins (e.g., PCR products of ORF's or total mRNA) may for example be attached to a solid support, hybridized with single stranded detectably-labeled cDNAs (corresponding to an “antisense” orientation), and quantified using an appropriate method such that a signal is detected at each location at which hybridization has taken place. The intensity of the signal would then reflect the level of gene expression. Comparison of results from viruses, for example, of different strains or from different samples or subjects, would elucidate differing levels of expression of specified genes. Using similar techniques, homologous nucleic acids may be identified from different viruses if SARS virus nucleic acids are used in the microarray, and probed with nucleic acid molecules from different viruses or subjects. In some embodiments, this approach may involve constructing his-tagged ORF expression libraries of viral genomes in a bacterial host, similar to an expression library in yeast (Martzen M. R. et al., 1999. Science, 286:1153). ORF-encoded protein activities may for example be detected in purified his-tagged protein pools in cases where activities cannot be detected in extracts or cells. In one aspect of the invention, arrayed libraries may be constructed of viral strains each of which bears a plasmid expressing a different SARS virus ORF under control of an inducible promoter. ORFs are amplified using PCR and cloned into a vector that enables their expression as N-terminal his-tagged polypeptides. These amplicons are also used to construct hybridization microarrays and enable targeted gene disruption, reducing expenses. A suitable expression host is selected, and genes encoding

particular biochemical activities are identified by screening arrayed pools of his-tagged proteins as described previously (Martzen M. R., McCraith S. M., Spinelli S.L., Torres F. M., Fields S., Grayhack E.J., and Phizicky E. M., 1999. *Science*, 286:1153).

In some embodiments, protein arrays (including antibody or antigen arrays) may be used for the analysis and identification of SARS virus polypeptides or host responses to such polypeptides. Thus, protein arrays may be used to detect SARS virus polypeptides in a patient; distinguish a SARS virus polypeptide from a host polypeptide; detect interactions between SARS virus polypeptides and for example host proteins; determine the efficacy of potential therapeutics, such as small molecules or ligands that may bind SARS virus polypeptides; determine protein-antibody interactions; and/or detect the interaction of enzyme-substrate interactions. Protein arrays may also be used to detect SARS virus antigens and antibodies in samples; to profile expression of SARS virus polypeptides; to identify suitable antibodies or map epitopes; or for a variety of protein function analyses.

A variety of methods are known for making and using microarrays, as for example disclosed in Cheung V. G., *et al.*, 1999. *Nature Genetics Supplement*, 21:15-19; Lipshutz R. J., *et al.*, 1999. *Nature Genetics Supplement*, 21:20-24; Bowtell D. D. L., 1999. *Nature Genetics Supplement*, 21:25-32; Singh-Gasson S., *et al.*, 1999. *Nature Biotechnol.*, 17:974-978; and Schweitzer B., *et al.*, 2002. *Nature Biotechnol.*, 20:359-365. Thus, for example, microarrays may be designed by synthesizing oligonucleotides with sequence variations based on a reference sequences, such as any SARS virus sequences described herein. Methods for storing, querying and analyzing microarray data have for example been disclosed in, for example, United States Patent No. 6,484,183; United States Patent No. 6,188,783; and Holloway A. J., *et al.*, 2002. *Nature Genetics Supplement*, 32:481-489. Protein arrays may be constructed, detected, and analysed using methods known in the art for example mass spectrometric techniques, immunoassays such as ELISA and western (dot) blotting combined with for example fluorescence detection techniques, and adapted for high throughput analysis, as described in for example MacBeath, G. and Schreiber, S.L. *Science* 2000, 289, 1760-1763; Levit-Binnun N, *et al.* (2003) Quantitative detection of protein arrays. *Anal Chem* 75:1436-41; Kukar T, *et al.* (2002) Protein microarrays to detect protein-protein interactions using red and green fluorescent proteins. *Anal Biochem* 306:50-4;

Borrebaeck CA, et al. (2001) Protein chips based on -recombinant antibody fragments: a highly sensitive approach as detected by mass spectrometry. *Biotechniques* 30:1126-1132; Huang RP (2001) Detection of multiple proteins in an antibody-based protein microarray system. *J Immunol Methods* 255:1-13; Emili AQ and Cagney G (2000) Large-scale functional analysis using peptide or protein arrays. *Nature Biotechnol* 18:393-397; Zhu H, et al. (2000) Analysis of yeast protein kinases using protein chips. *Nature Genet* 26:283-9; Lueking A, et al. (1999) Protein Microarrays for Gene Expression and Antibody Screening. *Anal. Biochem.* 270:103-111; or Templin MF, et al. (2002) Protein microarray technology. *Drug Discov Today* 7:815-822. Tools for microarray techniques are available commercially from for example Affymetrix, Santa Clara, CA; Nanogen, San Diego, CA; or Sequenom, San Diego, CA.

Computer Readable Records

Nucleic acid and polypeptide sequences, as described herein, or a fragment thereof, may be provided in a variety of media to facilitate access to these sequences and enable the use thereof. According, SARS virus nucleic acid and polypeptide sequences of the invention may be recorded or stored on computer readable media, using any technique and format that is appropriate for the particular medium.

In alternative embodiments, the invention provides computer readable media encoded with a number of distinct nucleic acid or amino acid data sequences of the invention. The number of distinct sequences may for example be any integer between 2 and 1×10^5 , such as at least 10^2 , 10^3 , 10^4 , or 10^5 . In one embodiment, the invention features a computer medium having a plurality of digitally encoded data records. Each data record may include a value representing a nucleic acid or amino acid sequence of the invention. In some embodiments, the data record may further include values representing the level of expression, level or activity of a nucleic acid or amino acid sequence of the invention. The data record can be structured as a table, for example, a table that is part of a database such as a relational database (for example, a SQL database of the Oracle or Sybase database environments). The invention also includes a method of communicating information about a sample, for example by transmitting information, for example transmitting a computer readable record as described herein, for example over a computer network. The polypeptide and nucleic acid sequences of

the invention, and sequence information pertaining thereto, may be routinely accessed by one of ordinary skill in the art for a variety of purposes, including for the purposes of comparing substantially identical sequences, etc. Such access may be facilitated using publicly available software as described herein. By "computer readable media" is meant any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

Pharmaceutical and Veterinary Compositions, Dosages, And Administration

Compounds of the invention can be provided alone or in combination with other compounds (for example, small molecules, peptides, or peptide analogues), in the presence of a liposome, an adjuvant, or any pharmaceutically acceptable carrier, in a form suitable for administration to humans or to animals.

Conventional pharmaceutical practice may be employed to provide suitable formulations or compositions to administer the compounds to patients suffering from or presymptomatic for SARS. Any appropriate route of administration may be employed, for example, parenteral, intravenous, subcutaneous, intramuscular, intracranial, intraorbital, ophthalmic, intraventricular, intracapsular, intraspinal, intracisternal, intraperitoneal, intranasal, aerosol, or oral administration. In some embodiments, compounds are delivered directly to the lung, by for example, formulations suitable for inhalation. In some embodiments, gene therapy techniques may be used for administration of SARS virus nucleic acid molecules, for example, as DNA vaccines. Formulations may be in the form of liquid solutions or suspensions; for oral administration, formulations may be in the form of tablets or capsules; and for intranasal formulations, in the form of powders, nasal drops, or aerosols.

Methods well known in the art for making formulations are found in, for example, "Remington's Pharmaceutical Sciences" (18th edition), ed. A. Gennaro, 1990, Mack Publishing Company, Easton, Pa. Formulations for parenteral administration may, for example, contain excipients, sterile water, or saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated naphthalenes.

Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Other potentially useful parenteral delivery systems for modulatory compounds include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation may contain excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or may be oily solutions for administration in the form of nasal drops, or as a gel.

If desired, treatment with a compound according to the invention may be combined with more traditional therapies for the disease.

For therapeutic or prophylactic compositions, the compounds are administered to an individual in an amount sufficient to stop or slow the replication of the SARS virus, or to confer protective immunity against future SARS virus infection. Amounts considered sufficient will vary according to the specific compound used, the mode of administration, the stage and severity of the disease, the age, sex, and health of the individual being treated, and concurrent treatments. As a general rule, however, dosages can range from about 1 μ g to about 100 mg per kg body weight of a patient for an initial dosage, with subsequent adjustments depending on the patient's response, which can be measured, for example by determining the presence of SARS nucleic acid molecules, polypeptides, or virions in the patient's peripheral blood.

In the case of vaccine formulations, an immunogenically effective amount of a compound of the invention can be provided, alone or in combination with other compounds, with an adjuvant, for example, Freund's incomplete adjuvant or aluminum hydroxide. The compound may also be linked with a carrier molecule, such as bovine serum albumin or keyhole limpet hemocyanin to enhance immunogenicity.

In general, compounds of the invention should be used without causing substantial toxicity. Toxicity of the compounds of the invention can be determined using standard techniques, for example, by testing in cell cultures or experimental animals and determining the therapeutic index, i.e., the ratio between the LD50 (the dose lethal to 50% of the population) and the LD100 (the dose lethal to 100% of the population). In some circumstances however, such as in severe disease conditions, it may be necessary to administer substantial excesses of the compositions.

Virus Isolation

Virus isolation was performed on a bronchoalveolar lavage specimen of a fatal SARS case belonging to the original case cluster from Toronto, Canada. All work with the infectious agent was performed in a biosafety level 3 (BSL3) laboratory using a N100 mask for personal protection. Samples were removed from BSL3 after addition of the RNA extraction buffer. The virus isolate, named the "Tor2 isolate" was grown in African Green Monkey Kidney (Vero E6) cells, the viral particles were purified, and the genetic material (RNA) was extracted from the Tor2 isolate (Poutanen, S. M. et al., N Engl J Med, Apr 10, 2003). More specifically, one hundred microlitre specimens were used to inoculate Vero E6 cells (ATCC CRL 1586) on Dulbecco's Modified Eagle Medium supplemented with penicillin/ streptomycin, glutamine and 2% fetal calf serum. The culture was incubated at 37°C. Cytopathogenic effect was observed 5 days post inoculation. The virus was passaged into newly seeded Vero E6 cells which showed a cytopathogenic effect as early as 2 days post infection (multiplicity of infection 10^{-2}). A virus stock was prepared from passage 2 of these cells and preserved in liquid nitrogen. The titer of the virus stock was determined to be 1×10^7 plaque forming units (p.f.u.) by plaque assay and 5×10^6 by tissue culture infectious dose (TCID) 50.

For virus propagation, 10 x T-162 flasks of Vero E6 cells were infected with a multiplicity of infection of 10^{-2} . When infected cells showed a cytopathogenic effect of '4+' (48 hours post infection), the cultures were then frozen and thawed to lyse the cells, and the supernatants were clarified from cell debris by centrifugation at 10,000 rpm in a Beckman high-speed centrifuge. The supernatants were treated with DNase and RNase for 3 hours at 37°C to remove any cellular genomic nucleic acids and subsequently extracted with an equal volume of 1,1,2-trichloro-trifluoroethane. The top fraction was ultra-centrifuged through a 5% / 40% glycerol step gradient at 151,000 x g for 1 hour at 4°C. The virus pellet was resuspended in PBS. RNA was isolated using a commercial kit from QIAGEN and stored at -80°C for further use.

cDNA Library Construction

The RNA and subsequent products were handled under biosafety level 2 (BSL2) conditions. The RNA sample was converted to a cDNA library, using a combined random-priming and oligo-dT priming strategy, and resultant subgenomic clones were processed under level 1 biosafety conditions. More specifically, purified viral RNA (55 ng) was used in the construction of a random primed and oligo-dT primed cDNA library, using the SuperScript Choice System for cDNA synthesis (Invitrogen). Linkers 5' -AATTCGCGGCCGCGTCGAC-3', SEQ ID NO: 195, and 5'-pGTCGACGCGGCCGCG-3', SEQ ID NO: 196, were ligated following cDNA synthesis. The cDNA synthesis products were visualized on agarose gels, revealing the anticipated low-yield smear. To produce sufficient cDNA for cloning, the cDNA product was size fractionated on a low-melting point preparative agarose gel, followed by PCR amplification using a single PCR primer 5'AATTCGCGGCCGCGTCGAC-3', SEQ ID NO: 197, specific to the linkers. This yielded sufficient material for cloning.

Size-selected cDNA products were cloned and single sequence reads were generated from each end of the insert from randomly picked clones. A list of the SARS virus clones is provided in the accompanying sequence listing, which is incorporated by reference herein (SEQ ID NOs: 92-159, 208 and 209).

More specifically, size-selected cDNAs were ligated into the pCR4-TOPO TA cloning vector (Invitrogen, CA), or after digestion with the restriction nuclease Not I into the pBR194c vector (The Institute for Genomic Research, Rockville, MD, USA). Ligated clones were then transformed by electroporation into DH10B T1 cells (Invitrogen), plated on 22 cm agar plates with the appropriate antibiotic and grown for 16 hours at 37°C. Colonies were picked into 384-well Axygen culture blocks containing 2 X YT media and grown in a shaking incubator for 18 hours at 37°C. Cells were lysed and DNA purified using standard laboratory procedures. Sequencing primers for the 194c clones were 5'-GGCCTCTTCGCTATTACGC-3' (forward primer) and 5' TGCAGGTCGACTCTAGAGGAT-3' (reverse primer).

DNA Sequencing And Assembly Of Reads

Sequences were assembled and the assembly edited to produce the genomic sequence of the SARS virus. More specifically, DNA sequencing of both ends of the plasmid templates was achieved using Applied Biosystems BigDye terminator reagent

(version 3), with electrophoresis and data collection on AB 3700 and 3730 XL instruments. DNA sequence reads were screened for non-viral contaminating sequences, trimmed for quality using PHRED (Ewing, B, and P. Green, *Genome Res* 8, 186-94, Mar, 1998) and assembled using PHRAP (Gordon, D. et al. *Genome Res* 8, 195-202, Mar, 1998). Simultaneously, sequences were used in BLAST searches of viral nucleotide and non-redundant protein datasets (NCBI, National Library of Medicine) to search for similarities. Sequence assemblies were visualized using CONSED (Gordon, D. et al. *Genome Res* 8, 195-202, Mar, 1998). Sequence mis-assemblies and contig joins were identified using Miropeats (Parsons, J. D., *Comput Appl Biosci* 11, 615-9 (Dec, 1995). As sequence data accrued, the additional sequences were assembled until it became apparent that the additional depth of sampling was increasing depth of coverage but not extending the length of the contig. At this point, 3,080 sequencing reads were generated, 2,634 of which were assembled into a single large contig.

The sequence information was imported into an ACEDB database (Durbin, J. Thierry-Mieg. 1991-. A *C. elegans* Database. Documentation, code and data available from anonymous FTP servers at lirmm.lirmm.fr, cele.mrc-lmb.cam.ac.uk and ncbi.nlm.nih.gov) and subjected to biological analysis including the identification of open reading frames, detection of similar sequences by BLAST and searching for apparent frameshifts. When frameshifts were identified by this analysis, the sequence assembly was consulted for evidence of sequencing errors and if found, they were corrected. The sequences were also searched for any that could extend the 5' end of the sequence and these were incorporated when found. High quality sequence discrepancies between different sequence reads were identified and resolved. Sequence reads classified as deleted or chimeric were identified through manual inspection and removed from the assembly. The resulting sequence has an average PHRED consensus quality score of 89.96. The lowest quality bases in the assembly are in the immediate vicinity of the 5' and 3' ends of the viral genome, with the lowest quality base having a PHRED score of 35. Most (29,694 of the 29,736 (99.86%)) of the bases have a consensus score of 90. Almost all regions of the genome are represented by reads derived from both strands of the plasmid sequencing templates, the exceptions being 50 bases at the 5' end represented by a single sequencing read, and 5 bases at the 3' end

represented by a single read. The average base in the assembly is represented by 30 reads in the forward direction and 30 reads in the reverse direction, as determined by PHRED. RT-PCR products predicted from the sequence and spanning the entire genome yield PCR products of the anticipated size on agarose gels. To confirm the 5' end of the viral genome RACE was performed using the RLM-RACE kit from Ambion, and primers 5'-CAGGAAACAGCTATGACACCAAGAACAAGGCTCTCCA-3' (SEQ ID NO: 90) and 5'-CAGGAAACAGCTATGACGATAGGGCCTCTTCCACAGA-3' (SEQ ID NO: 91). Fourteen clones were recovered and sequenced. Analysis of these sequences confirmed the 5' end of the coronavirus genome. The SARS genomic sequences have been deposited into Genbank (Accession Nos. AY274119.1, AY274119.2, and AY274119.3).

While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure that come within known or customary practice within the art to which the invention pertains, and may be applied to the essential features set forth herein and in the scope of the appended claims.

All patents, patent applications, and publications referred to herein are hereby incorporated by reference in their entirety to the same extent as if each individual patent, patent application, or publication was specifically and individually indicated to be incorporated by reference in its entirety.

What is claimed is:

1. A substantially pure SARS virus nucleic acid molecule.
- 5 2. The molecule of claim 1, wherein said molecule is selected from the group consisting of genomic RNA or DNA, cDNA, synthetic DNA, or mRNA.
3. The molecule of claim 1 or 2, wherein said molecule comprises a sequence substantially identical to a sequence selected from the group consisting of SEQ ID
10 NOs: 1-13, 15-18, 20-30, 90-159, 208, and 209 or a fragment thereof.
4. The molecule of claim 3, wherein said molecule comprises a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO:2, and SEQ ID NO: 15 or a
15 fragment thereof.
5. The molecule of claim 3, wherein said molecule comprises a sequence substantially identical to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO:2, and SEQ ID NO: 15, or a fragment thereof.
- 20 6. The molecule of any one of claims 1 through 3, wherein said molecule comprises a s2m motif.
7. The molecule of claim 6, wherein said s2m motif comprises a sequence substantially identical to a sequence selected from the group consisting of SEQ ID
25 NOs: 16, 17, and 18.
8. The molecule of any one of claims 1 through 3, wherein said molecule comprises a leader sequence.
- 30 9. The molecule of claim 8, wherein said leader sequence comprises a sequence substantially identical to the sequence of SEQ ID NO: 3.

10. The molecule of any one of claims 1 through 3, wherein said molecule comprises a transcriptional regulatory sequence.

11. The molecule of claim 10, wherein said transcriptional regulatory sequence
5 comprises a sequence substantially identical to the sequence selected from the group consisting of SEQ ID NOs: 4-13 and 20-30.

12. The molecule of claim 1, wherein said molecule comprises a sequence
substantially identical to a sequence selected from nucleotides 265-13,398; 13,398-
10 21,485; 21,492 – 25,259; 25,268 – 26,092; 25,689 – 26,153; 26,117 – 26,347; 26,398 –
27,063; 27,074 – 27,265; 27,273 – 27,641; 27,638 – 27,772; 27,779 – 27,898; 27,864 –
28,118; 28,120 – 29,388; 28,130 – 28,426; 28,583 – 28,795; and 29,590 – 29,621 of
SEQ ID NO: 15.

13. The molecule of any one of claims 1 through 3, wherein said molecule encodes
15 a polypeptide.

14. The molecule of any one of claims 1 through 3, wherein said molecule encodes
a polypeptide.

20 15. A substantially pure SARS virus polypeptide.

16. The polypeptide of claim 15, wherein said polypeptide comprises a polypeptide.

25 17. The polypeptide of claim 15, wherein said polypeptide comprises an identifiable
signal sequence.

18. The polypeptide of claim 17, wherein said signal sequence comprises a
30 sequence substantially identical to a sequence selected from the group consisting of
SEQ ID NOs: 76 and 85.

19. The polypeptide of claim 15, wherein said polypeptide comprises a transmembrane domain.
20. The polypeptide of claim 19, wherein said transmembrane domain comprises a
5 sequence substantially identical to a sequence selected from the group consisting of
SEQ ID NOs: 77-86.
21. The polypeptide of claim 15, wherein said polypeptide comprises a
glycoprotein.
10
22. The polypeptide of claim 21, wherein said glycoprotein comprises a matrix
glycoprotein.
23. The polypeptide of claim 22, wherein said matrix glycoprotein comprises a
15 sequence substantially identical to SEQ ID NO: 34.
24. The polypeptide of claim 15, wherein said polypeptide is selected from the
group consisting of a transmembrane protein and a multitransmembrane protein.
- 20 25. The polypeptide of claim 15, wherein said polypeptide is selected from the
group consisting of a type I transmembrane protein and a type II transmembrane
protein.
26. The polypeptide of claim 24, wherein said polypeptide comprises a
25 transmembrane anchor or a a transmembrane helix.
27. The polypeptide of any one of claims 1 through 3, wherein said polypeptide
comprises an epitope of a SARS virus
28. The polypeptide of claim 15, wherein said polypeptide comprises an ATP-
30 binding domain.

29. The polypeptide of claim 15, wherein said polypeptide comprises a viral envelope protein.

5 30. The polypeptide of claim 15, wherein said polypeptide comprises a nuclear localization signal.

31. The polypeptide of claim 15, wherein said polypeptide comprises a lysine-rich sequence.

10 32. The polypeptide of claim 31, wherein said lysine-rich sequence comprises a sequence substantially identical to SEQ ID NO: 14.

15 33. The polypeptide of claim 15, wherein said polypeptide comprises a RNA binding protein.

34. The polypeptide of claim 15, wherein said polypeptide comprises a hydrophilic domain.

20 35. The polypeptide of claim 34, wherein said hydrophilic domain comprises a sequence substantially identical to SEQ ID NO: 87.

25 36. The polypeptide of claim 15, wherein said polypeptide is selected from the group consisting of replicase 1a, replicase 1b, spike glycoprotein, small envelope protein, matrix glycoprotein, and nucleocapsid protein.

37. The polypeptide of claim 15, wherein said polypeptide comprises a sequence substantially identical to a sequence selected from the group consisting of SEQ ID NOs: 14, 33-36, 64-74, and 76-87 or a fragment thereof.

30 38. A vector comprising the nucleic acid molecule of claim 1.

39. The vector of claim 38, wherein said vector comprises a sequence substantially identical to a sequence selected from the group consisting of SEQ ID NOs: 1-13, 15-18, 20-30, 90-159, 208, and 209.

5 40. The vector of claim 38, wherein said vector is a gene therapy vector.

41. A host cell comprising the vector of claim 38.

42. The host cell of claim 41, wherein said cell is selected from the group consisting
10 of a mammalian cell, a yeast, a bacterium, and a nematode cell.

43. A nucleic acid molecule having substantial nucleotide sequence identity to a
sequence encoding a SARS virus polypeptide or fragment thereof, wherein said
fragment comprises at least six amino acids, and wherein said nucleic acid molecule
15 hybridizes under high stringency conditions to at least a portion of a SARS virus
nucleic acid molecule.

44. The nucleic acid molecule of claim 43, wherein said nucleic acid molecule has
100% sequence complementarity to said sequence encoding a SARS virus polypeptide
20 or fragment thereof.

45. A nucleic acid molecule having substantial nucleotide sequence identity to a
SARS virus nucleotide sequence, wherein said nucleic acid molecule comprises at least
ten nucleotides, and wherein said nucleic acid molecule hybridizes under high
25 stringency conditions to at least a portion of a SARS virus nucleic acid molecule.

46. The nucleic acid molecule of claim 45, wherein said nucleic acid molecule has
100% sequence complementarity to said SARS virus nucleotide sequence.

30 47. A nucleic acid molecule comprising a sequence that is antisense to a SARS
virus nucleic acid molecule

48. An antibody that specifically binds to a SARS virus polypeptide.

49. The antibody of claim 48, wherein said antibody is a neutralizing antibody.

5 50. A method for detecting a SARS virus virion or polypeptide in a sample, said method comprising contacting said sample with the antibody of claim 48, and determining whether said antibody specifically binds to said polypeptide.

10 51. A method for detecting a SARS virus genome or gene or homolog or fragment thereof in a sample, said method comprising contacting a SARS virus nucleic acid molecule, wherein said nucleic acid molecule comprises at least ten nucleotides, with a preparation of DNA from said sample, under hybridization conditions providing detection of DNA sequences having nucleotide sequence identity to a SARS virus nucleic acid molecule.

15

52. The method of claim 31, wherein said nucleic acid molecule comprises at least one of a primer pair, wherein said primer pair hybridizes to said a SARS virus genome or gene or homolog or fragment thereof under conditions suitable for polymerase chain reaction.

20

53. A method of targeting a protein for secretion from a cell, said method comprising attaching a signal sequence from a SARS virus polypeptide to said protein, such that said protein is secreted from said cell.

25 54. A nucleic acid molecule comprising a sequence complementary to a SARS virus nucleotide sequence.

30 55. A kit for detecting the presence of a SARS virus nucleic acid molecule or polypeptide in a sample, said kit comprising a reagent selected from the group consisting of a SARS virus nucleic acid molecule and an antibody that specifically binds a SARS virus polypeptide.

56. A method for eliciting an immune response in an animal, said method comprising identifying an animal infected with or at risk for infection with a SARS virus, and administering a SARS virus polypeptide or fragment thereof, or administering a SARS virus nucleic acid molecule encoding a SARS virus polypeptide or fragment thereof, to said animal.
57. The method of claim 56, wherein said administering results in the production of an antibody in said animal.
58. The method of claim 56, wherein said administering results in the generation of cytotoxic or helper T-lymphocytes in said animal.
59. A method for treating or preventing a SARS virus infection comprising identifying an animal infected with or at risk for infection with a SARS virus, and administering a SARS virus nucleic acid molecule or polypeptide, or administering a compound that inhibits pathogenicity or replication of a SARS virus, to the animal.
60. The method of claim 59, wherein the animal is a human.
61. Use of a SARS virus nucleic acid molecule or polypeptide for treating or preventing a SARS virus infection.
62. A method of identifying a compound for treating or preventing a SARS virus infection, comprising contacting sample comprising a SARS virus nucleic acid molecule or contacting a SARS virus polypeptide with the compound, wherein an increase or decrease in the expression or activity of the nucleic acid molecule or the polypeptide identifies a compound for treating or preventing a SARS virus infection.
63. A vaccine comprising a SARS virus nucleic acid molecule or polypeptide.
64. The vaccine of claim 62, wherein the vaccine is a DNA vaccine.

65. A microarray comprising a plurality of elements, wherein each element comprises one or more distinct nucleic acid or amino acid sequences, and wherein the sequences are selected from a SARS virus nucleic acid molecule or polypeptide, or an antibody that specifically binds a SARS virus nucleic acid molecule or polypeptide.

5

66. A computer readable record comprising distinct SARS virus nucleic acid or amino acid sequences.

10

67. The computer readable record of claim 65, wherein the computer readable record comprises a database.

Replicase 1A

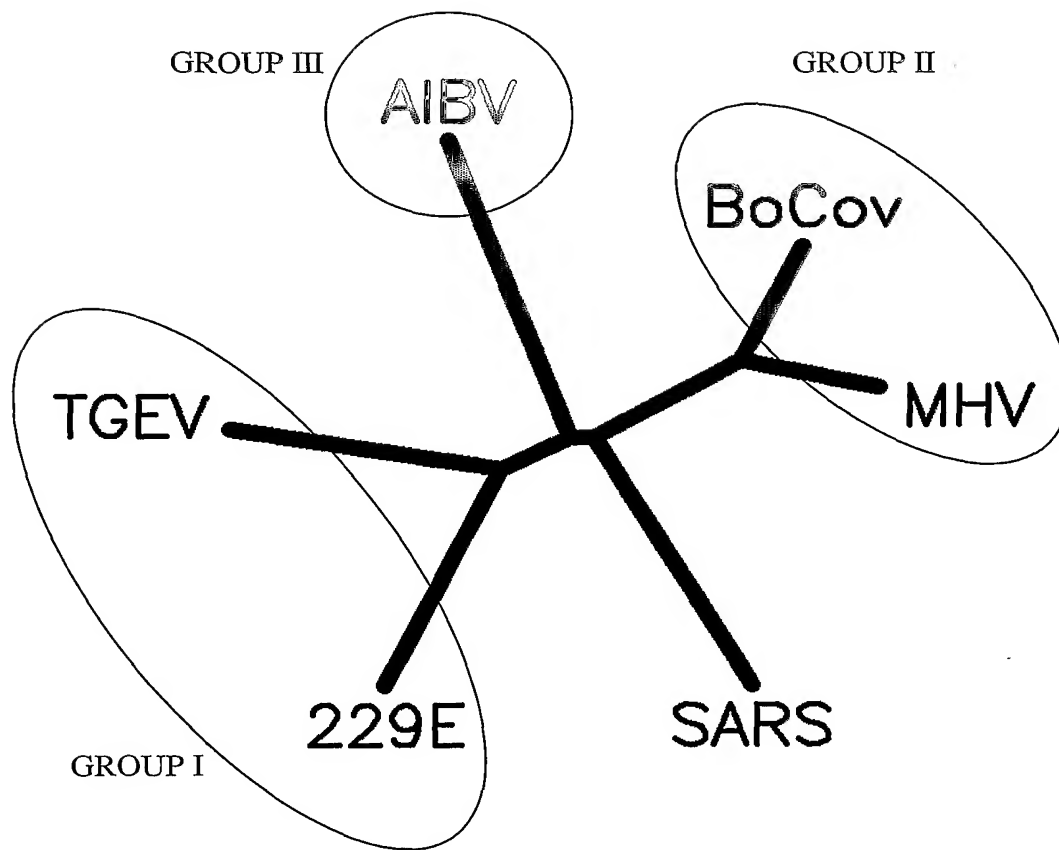


Figure 1A

Matrix Glycoprotein M

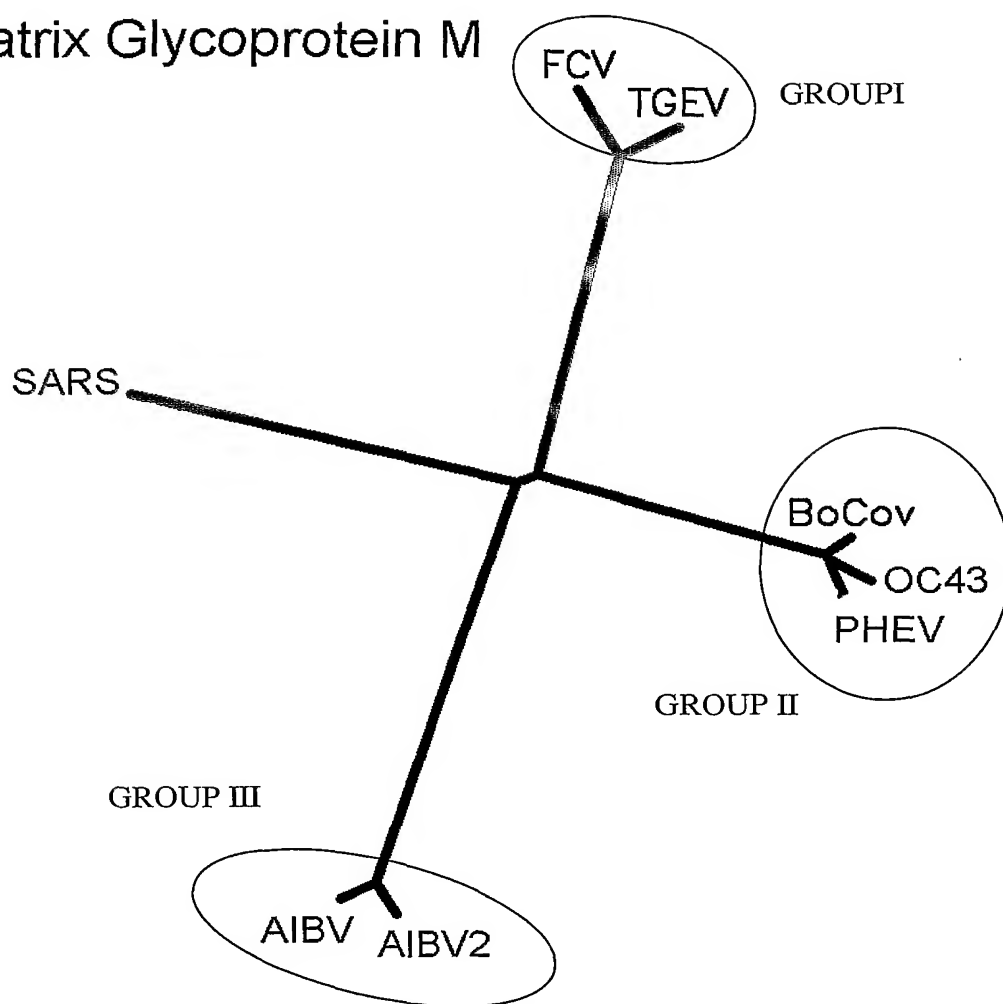


Figure 1B

Nucleocapsid

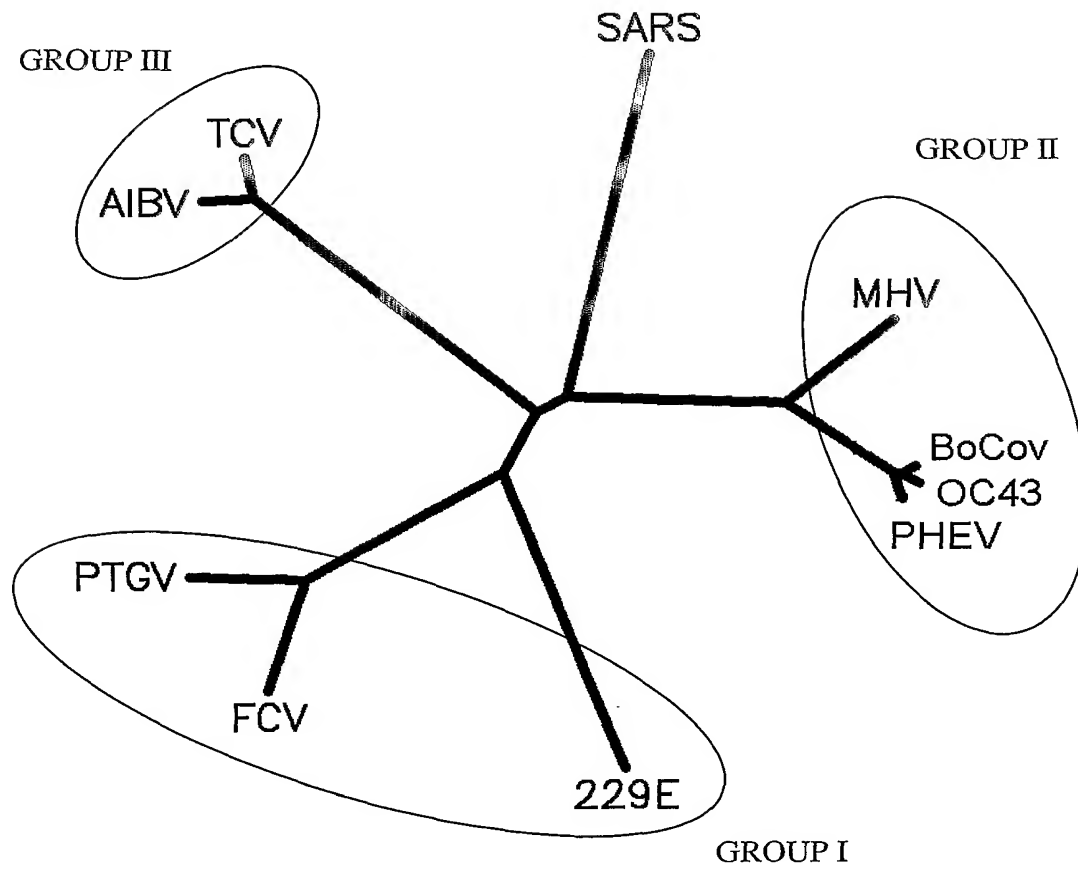


Figure 1C

S (Spike) Glycoprotein

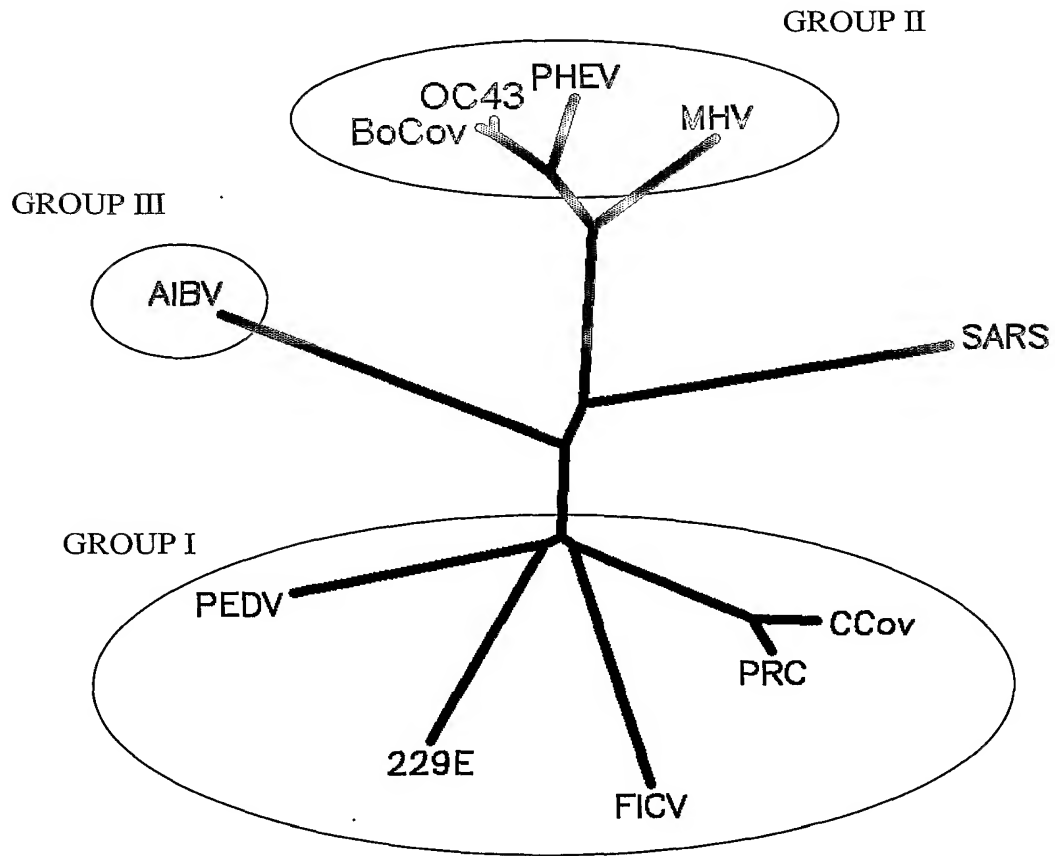


Figure 1D

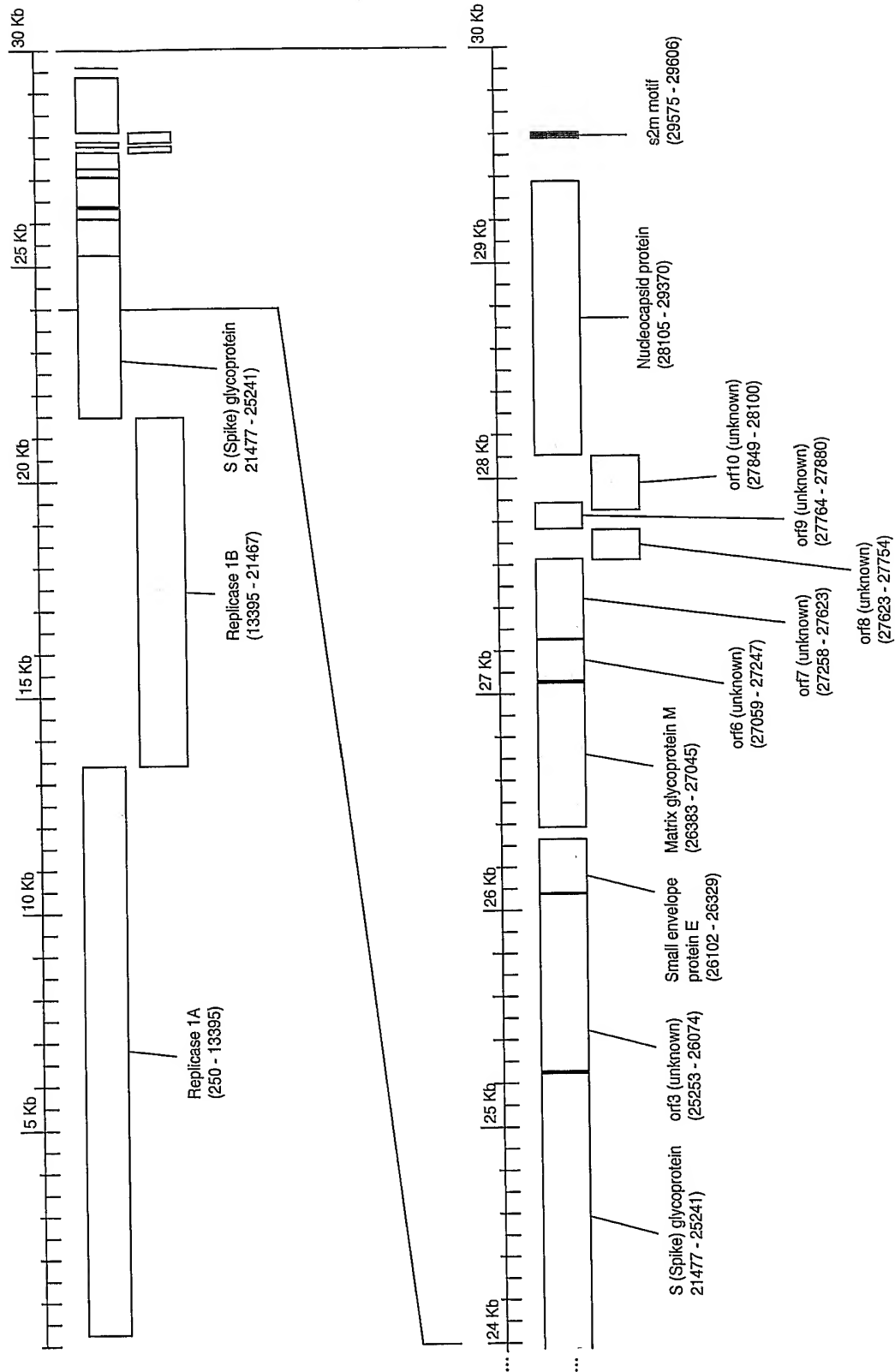


Figure 2

CTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTTCTCTAAACGAACTTTAAAATCTGTGT
AGCTGTGCTCGCTCGGCTGCATGCCTAGTGCACCTACGCAGTATAACAATAATAAATTTTACTGTGCTTGACA
AGAAACGAGTAACCTCGTCCCTCTTCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCA
TACCTAGGTTTTCTGTCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTCTTGGTGTCAACGAGAAAAC
ACACGTCCAACCTCAGTTTGCCGTGCTTTCAGGTTAGAGACGTGCTAGTGCCTGGCTTCGGGGACTCTGTGG
AAGAGGCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGTCTAGTAGAGCTGGAAGGAGGC
GTACTGCCCCAGCTTGAACAGCCCTATGTGTTTCATTAAACGTTCTGATGCCCTAAGCACCAATCACGGCCA
CAAGGTGCTTGAGTTGGTTGCAGAAATGGACGGCATTACGTACGGTCTAGCGGTATAACACTGGGAGTAC
TCGTGCCACATGTGGGCGAAACCCCAATTGCATACCGCAATGTTCTTCTTCTGTAAGAACGGTAATAAGGGA
GCCGGTGGTCTAGCTATGGCATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGATCCCAT
TGAAGATTATGAACAAAACCTGGAACACTAAGCATGGCAGTGGTGCACCTCCGTGAACCTCACTCGTGAGCTCA
ATGGAGGTGCAGTCACTCGCTATGTGCGACAACAATTTCTGTGGCCAGATGGGTACCCTCTTGATTGCATC
AAAGATTTTTCTGCGACGCGCGGGCAAGTCAATGTGCACTCTTTCCGAACAACCTTGATTACATCGAGTCGAA
GAGAGGTGTCTACTGCTGCCGTGACCATGAGCATGAAATTGCCTGGTTCCTGAGCGCTCTGATAAGAGCT
ACGAGCACCAGACACCCCTTCGAAATTAAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAG
TTTGTGTTTCTCTTAACCTCAAAGTCAAAGTCAATTCACACCGTGTGAAAAGAAAAGACTGAGGGTTT
CATGGGGCGTATACGCTCTGTGTACCTGTTGCATCTCCACAGGAGTGTAAACAATATGCACCTGTCTACCT
TGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAGACGTGCGACTTTCTGAAAGCCACTTGTGAACAT
TGTGGCACTGAAAATTTAGTTATTTGAAGGACCTACTACATGTGGGTACCTACCTACTAATGCTGTAGTGAA
AATGCCATGTCTGCTGTCAAGACCCAGAGATTGGACCTGAGCATAGTGTTCAGATTATCACAACCACT
CAAACATTGAAACTCGACTCCGCAAGGGAGGTAGGACTAGATGTTTGGAGGCTGTGTGTTGCTATGTT
GGCTGCTATAATAAGCGTGCTTACTGGGTTCTCGTGCTAGTGCTGATATTGGCTCAGGCCATACTGGCAT
TACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGAACGTGTTAACATTA
ACATTGTTGGCGATTTTCATTTGAATGAAGAGGTTGCCATCATTTTGGCATCTTTCTCTGCTTCTACAAGT
GCCTTTATTGACACTATAAAGAGTCTTGATTACAAGTCTTTCAAACCATTTGTTGAGTCTGCGGTAACATA
TAAAGTTACCAAGGGGAAAGCCCGTAAAAGGTGCTTGGAAACATTGGACAACAGAGATCAGTTTAAACACCAC
TGTGTGGTTTTTCCCTCACAGGCTGCTGGTGTATCAGATCAATTTTTGCGCGCACACTTGATGCAGCAAAAC
CACTCAATTCCTGATTTGCAAAGAGCAGCTGTCAACATACTTGATGGTATTTCTGAACAGTCATTACGTCT
TGTCGACGCCATGGTTTATACCTCAGACCTGCTCACCAACAGTGTCATTATTATGGCATATGTAACCTGGTG
GTCTTGTACAACAGACTTCTCAGTGGTTGTCTAATCTTTTGGGCACTACTGTTGAAAACCTCAGGCCATC
TTTGAATGGATTGAGGCGAAACTTAGTGACAGGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAAT
TCTCATTACAGGTGTTTTTGACATCGTCAAGGGTCAAATACAGGTGCTTCAGATAACATCAAGGATTGTG
TAAAATGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAAGTCACATATCGCTGGCGCA
AAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAAAGCAAGGGACTTTACCGTCAGTGATACG
TGGCAAGGAGCAGCTGCAACTACTCATGCTCTTAAGGCACAAAAGTAACCTTTCTTGAAGGTGATGAT
CACATGACACAGTACTTACCTCTGAGGAGGTTGTTCTCAAGAACGGTGAACCTCGAAGCACTGAGACGCCC
GTTGATAGCTTCACAAATGGAGCTATCGTCGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAGAT
TAAGGACAAAGAACAATACTGCGCATTTGTCTCCTGGTTTACTGGCTACAAACAATGTCTTTGCTTAAAAG
GGGGTGCACCAATTAAGGTGTAACCTTTGGAGAAGATACTGTTTGGGAAGTTCAAGGTTACAAGAATGTG
AGAATCACATTTGAGCTTGATGAACGTGTTGACAAAGTGCTTAATGAAAAGTGCTCTGTCTACACTGTTGA
ATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCAGAGGCTGTTGTGAAGACTTTACAACCAGTTT
CTGATCTCCTTACCAACATGGGTATTTGATCTTGATGAGTGGAGTGTAGCTACATTTCTACTTATTTGATGAT
GCTGGTGAAGAAAACCTTTTCATCACGTATGTATTGTTTCTTTTACCCTCCAGATGAGGAAGAAGAGGACGA
TGCAGATGTGAGGAAGAAGAAATTTGATGAAACCTGTGAACATGAGTACGGTACAGAGGATGATTATCAAG
GTCTCCCTCTGGAATTTGGTGCTCAGCTGAAACAGTTTCGAGTTGAGGAAGAAGAAGAGGAAGACTGGCTG
GATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAGAACCTACACCTGAAGAACCAGTTAATCAGTT
TACTGGTTATTTAAAACCTTACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTG
CTAATCCTATGGTGATTGTAAATGCTGCTAACATAACCTGAAACATGGTGGTGGTGTAGCAGGTGCACTC
AACAAGGCAACCAATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAATGGCCCTCTTACAGT
AGGAGGGTCTTGTGTTGCTTTCTGGACATAATCTTGCTAAGAAGTGCTGCTGATGTTGTTGGACCTAACCTAA
ATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCATATGAAAATTTCAATTCACAGGACATCTTACTTGCA
CCATTGTTGTGACAGGCATATTTGGTGCTAAACCACTTCACTGCTTTACAAGTGTGCGTGCAGACGGTTCG
TACACAGGTTTATATTGACGTCAATGACAAAGCTCTTTATGAGCAGGTTGTGATGGATTATCTTGATAACC
TGAAGCTAGAGTTGGAAGCACCTAAACAAGAGGAGGCCACCAACACAGAAGATTCCAAAACCTGAGGAGAAA
TCTGTGCTACAGAAGCCTGTGCGATGTGAAGCCAAAATTAAGGCCTGCATTGATGAGGTTACCACAACACT
GGAAGAACTAAGTTTCTTACCAATAAGTTACTCTTGTGTTGCTGATATCAATGGTAAGCTTTACCATGATT
CTCAGAACATGCTTAGAGGTGAAGATATGTCTTCTTCTGAGAAGGATGCACCTTACATGGTAGGTGATGTT

FIGURE 3A

ATCACTAGTGGTGATATCACTTGTGTTGTAATACCCTCCAAAAAGGCTGGTGGCACTACTGAGATGCTCTC
AAGAGCTTTGAAGAAAGTGCCAGTTGATGAGTATATAACCACGTACCTTGGACAAGGATGTGCTGGTTATA
CACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTACCTTCAGAAGCACCT
AATGCTAAGGAAGAGATTCTAGGAACGTATCCTGGAATTTGAGAGAAATGCTTGCTCATGCTGAAGAGAC
AAGAAAATTAATGCCTATATGCATGGATGTTAGAGCCATAATGGCAACCATCCAACGTAAGTATAAAGGAA
TTAAAATTCAGAGGGCATCGTTGACTATGGTGTCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCT
TCTATTATTACGAAGCTGAACCTCTCTAAATGAGCCGCTTGTGCACAATGCCAATTGGTTATGTGACACATGG
TTTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGCTCCTGCCGTAGTGTGAGTATCATCAC
CAGATGCTGTTACTACATATAATGGATACCTCACTTCGTGCATCAAAGACATCTGAGGAGCACTTTGTAGAA
ACAGTTTCTTTGGCTGGCTCTTACAGAGATTGGTCTTATTCAGGACAGCGTACAGAGTTAGGTGTTGAATT
TCTTAAGCGTGGTGACAAAATTTGTGTACCACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGG
TTCTTTCACTTGACAAACTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAAAAGTGTTTCACT
GTGGACAACACTAATCTCCACACACAGCTTGTGGATATGTCTATGACATATGGACAGCAGTTTGGTCCAAC
ATACTTGGATGGTGTGATGTTACAAAAATTAACCTCATGTAAATCATGAGGGTAAGACTTTCTTTGTAC
TACCTAGTAGTACACTACCTAGTAGTGAAGCTTTTCGAGTACTACCATACTCTTGATGAGAGTTTCTTGGT
AGGTACATGTCTGCTTTAAACCACACAAAGAAATGGAAATTTCCCTCAAGTTGGTGGTTAACTTCAATPAA
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CACCAGCACTTCAAGAGGCTTATTATAGAGCCCGTGTGGTGATGCTGCTAACTTTTGTGCACTCATACTC
GCTTACAGTAATAAACTGTTGGCGAGCTTGGTGATGTGAGAGAACTATGACCCATCTTCTACAGCATGC
TAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGTGGTCAGAAACTACTACCTTAA
CGGGTGATAGAAGCTGTGATGTATATGGGTACTCTATCTTATGATAATCTTAAGACAGGTGTTTCCATTCCA
TGTGTGTGTGGTGTGATGCTACACAATATCTAGTACAACAAGAGTCTTCTTTTGTATGATGTCTGCACC
ACCTGCTGAGTATAAATTACAGCAAGGTACATTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTG
GTCATTACACTCATATAACTGCTAAGGAGACCCCTCTATCGTATTGACGGAGCTCACCTTACAAGATGTCA
GAGTACAAGGACCATGACTGATGTTTCTACAAGAAACATCTTACACTACAACCATCAAGCCTGTGTC
GTATAAACTCGATGGAGTTACTTACACAGAGATTGAACCAAAATTTGGATGGGTATTATAAAAAGGATAATG
CTTACTATACAGAGCAGCCTATAGACCTTGTACCAACTCAACCATTACCAAATGCGAGTTTTGATAAATTC
AAACTCACATGTTCTAACACAAAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTC
ACGAGAGCTATCTGTCACATTTCTTCCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTATT
CAGCGAGTTTCAAGAAAGGTGCTAAATTAAGTGCATAAGCCAATTTGTTTGGCACATTAACCAGGCTACAACC
AAGACAACGTTCAAAACCAACACTTGGTGTTTACGTTGTCTTTGGAGTACAAAGCCAGTAGATACTTCAAA
TTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGAATGGACAATCTTGCTTGTGAAAGTCAACAACCCA
CCTCTGAAGAAGTAGTGGAATCCTACCATACAGAAGGAAGTCATAGAGTGTGACGTGAAAACCTACCGAA
GTTGTAGGCAATGTCACTTAAACCATCAGATGAAGGTGTTAAAGTAACACAAGAGTTAGGTGATGAGGA
TCTTATGGCTGCTTATGTGGAACACACAAGCATTACCAATTAAGAAACCTAATGAGCTTTCAGTCCCTTAG
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TAACAATTATATGCCTTATGTGTTTACATTATTGTTCCAATTGTGTACTTTTACTAAAAGTACCAATTCTA
GAATTAGAGCTTCACTACCTACAACATTGCTAAAATAGTGTTAAGAGTGTGCTAAATTATGTTTGGAT
GCCGGCATTAATTATGTGAAGTCACCCAAATTTTCTAAATTTGTTTCACAATCGCTATGTGGCTATTGTTGTT
AAGTATTTGCTTAGGTTCTCTAATCTGTGTAACGTGCTGCTTTTGGTGTACTCTTATCTAATTTTGGTGCTC
CTTCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTTCGTCTAACGTTACTACTATGGATTTCTGTGAA
GGTTCTTTTCTTGCAGCATTTGTTTAAAGTGGATTAGACTCCCTTGATTTCTTATCCAGCTCTTGAACCAT
TCAGGTGACGATTTTCATCGTACAAGCTAGACTTGACAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCAT
ATATGTTGTTTCAAAAATTTCTTTTATTATTAGGTCTTTTCAGCTATAATGCAGGTGTTCTTTGGCTATTTT
GCTAGTCATTTTCATCAGCAATTTCTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCACCCGTTTC
TGCAATGGTTAGGATGTACATCTTCTTTGCTTCTTTCTACTACATATGGAAGAGCTATGTTTCATATCATGG
ATGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGCAATCGTGCCACACGCGTTGAGTGTACAAC
ATTGTTAATGGCATGAAGAGATCTTCTATGTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAA
TTGGAATTGTCTCAATTGTGACACATTTTGCACCTGGTAGTACATTCATTAGTGTGAAGTTGCTCGTGATT
TGTCACCTCCAGTTTAAAAGACCAATCAACCCTACTGACCAGTCATCGTATATTGTTGATAGTGTGCTGTG
AAAAATGGCGCGCTTCACTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGACATCCGCTCTCCCA
TTTTGTCAATTTAGACAATTTGAGAGCTAACACACTAAAGGTTCACTGCCTATTAAATGTATAGTTTGTG
ATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAGCTGCTCTTCTGTGTACTACAGTCAAGTGTGTCGCA
CCTATTCTGTTGCTTGACCAAGCTCTTGTATCAGACGTTGGAGATAGTACTGAAGTTTCCGTTAAGATGTT
TGATGCTTATGTGACACCTTTTCAGCAACTTTTAGTGTTCTTATGGAAAACTTAAGGCACCTGTTGCTA
CAGCTCACAGCGAGTTAGCAAAGGGTGTAGCTTTAGATGGTGTCTTCTTACATTCGTGTGCTGCCCCGA

FIGURE 3B

CAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTCAAACCTTTCACATCACTCTGA
CTTAGAAGTGACAGGTGACAGTTGTAACAATTTTCATGCTCACCTATAATAAGGTTGAAAACATGACGCCCCA
GAGATCTTGCGCATGTATTGACTGTAATGCAAGGCATATCAATGCCCAAGTAGCAAAAAGTCACAATGTT
TCACTCATCTGGAATGTAAAAGACTACATGTCTTTATCTGAACAGCTGCGTAAACAAAATTCGTAGTGCTGC
CAAGAAGAACAACATACTTTTAGACTAACTTGTGCTACAACCTAGACAGGTTGTCAATGTCATAACTACTA
AAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTTGTTTTAAACTTATGCTTAAGGCCACATTATTGTGC
GTTCTTGCTGCATTGGTTTGGTTATATCGTTATGCCAGTACATACATTGTCAATCCATGATGGTTACACAAA
TGAAATCATTGGTTACAAAGCCATTACAGGATGGTGTCTACTCGTGACATCATTTCTACTGATGATTGTTTTG
CAAATAAACATGCTGGTTTTGACGCATGGTTTAGCCAGCGTGGTGGTTCATACAAAAATGACAAAAGCTGC
CCTGTAGTAGCTGCTATCATTACAAGAGAGATTGGTTTTCATAGTGCCTGGCTTACCGGGTACTGTGCTGAG
AGCAATCAATGGTGACTTCTTGCATTTTCTACCTCGTGTTTTTAGTGCTGTTGGCAACATTTGCTACACAC
CTTCCAACTCATTGAGTATAGTGATTTTGTCTACCTCTGCTTGCCTTCTGCTGCTGAGTGACAAATTTTT
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ATGAAATTCAGACGTGTTTTTGGTGAGTACAACCATGTTGTTGCTGCTAATGCATTTTGTTTTTTGATGTC
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TGACATTCATTTTACCAATGATGTTTCATTTCTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATT
GTGCTTTTTTGGATAACAGCAATCTATGTATTTCTGTATTTCTCTGAAGCACTGCCATTGGTTCCTTAAACA
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TATCTTGCTCTATATAACAAGTACAAGTATTTCACTGAGGAGCTTAGATACTACCAGCTATCGTGAAGCAGC
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GGGTGCATGGTACAAGTAACCTGTGGAACCTACAACCTTAAATGGATTGTGGTTGGATGACACAGTATACTG
TCCAAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCTAACTATGAAGATCTGCTCATTTCGCAAT
CCAACCATAGCTTTCTTGTTCAGGCTGGCAATGTTCAACTTCGTGTTATTGGCCATTCATGCAAAATTTGT
CTGCTTAGGCTTAAAGTTGATACTTCTAACCCCTAAGACACCCAAGTATAAAATTTGTCCGTATCCAACCTGG
TCAAACATTTTCACTTCTAGCATGCTACAATGGTTCACCATCTGGTGTATTCAGTGTTGCCATGAGACCTA
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GTGCTTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACACGCTGGTACTGACTTAGAAGGTAA
ATTCATATGGTCCATTTGTTGACAGACAACTGCACAGGCTGCAGGTACAGACACAACCATTAACATTAAATG
TTTTGGCATGGCTGTATGCTGCTGTTATCAATGGTGATAGGTGGTTTTCTTAATAGATTACCACTACTTTG
AATGACTTTAACTTGTGGCAATGAAGTACAACCTATGAACCTTTGACACAAGATCATGTTGACATATTGGG
ACCTCTTTCTGCTCAAACAGGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTGCAGAATG
GTATGAATGGTCGTACTATCCTTGGTAGCACTATTTTAGAAGATGAGTTTACACCATTGATGTTGTTAGA
CAATGCTCTGGTGTACCTTCCAAGGTAAGTTCAAGAAAATTTGTTAAGGGCACTCATCATTGGATGCTTTT
AACTTTCTTGACATCACTATTGATTCTTGTTCAAAGTACACAGTGGTCACTGTTTTTCTTTGTTTACGAGA
ATGCTTTCTTGCCATTTACTCTTGGTATTATGGCAATTGCTGCATGTGCTATGCTGCTTGTAAAGCATAAG
CACGATTCCTTGTGCTTGTGTTCTGTTACCTTCTCTGCAACAGTTGCTTACTTTAATATGGTCTACATGCC
TGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCTGGTTATAGGCTTA
AGGATTGTGTTATGTATGCTTCAGCTTTAGTTTTGCTTATTCTCATGACAGCTCGCACTGTTTATGATGAT
GCTGCTAGACGTGTTTGGACACTGATGAATGTCATTACACTTGTTTACAAAGTCTACTATGGTAATGCTTT
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ACCTTACAGTGTATCATGCTTGTATTGTTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGCCTTTTCTG
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GGTATTGGAGGTAAACCATGTATCAAGGTTGCTACTGTACAGTCTAAAATGTCTGACGTAAGATGCACATC
TGTGTTACTGCTCTCGGTTCTTCAACAACCTAGAGTAGAGTACATCTTCTAAATTTGTGGGCAACATGTGTAC
AAGCTTCAACATGATATTCTTCTTGCAAAAAGACACAACCTTCAAGCTTTTCGAGAAGATGGTTTTCTTTTGTCT
CTTTTGTCTATCCATGCAGGGTGTCTGTAGACATTAATAGGTTGTGCGAGGAAAATGCTCGATAACCGTGCTAC
TCTTCAAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCCGCTTATGCCACTGCCCAGGAGGCT
ATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTCGTTCTCAAAAAGTTAAAGAAATCTTTGAATGTGGCT

FIGURE 3C

AAATCTGAGTTTGACCGTGATGCTGCCATGCAACGCAAGTTGGAAAAGATGGCAGATCAGGCTATGACCCA
AATGTACAAACAGGCAAGATCTGAGGACAAGAGGGCAAAAGTAAGTACTAGTGCTATGCAAACAATGCTCTTCA
CTATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGTTGTGTTCCA
CTCAACATCATACCATTGACTACAGCAGCCAACTCATGGTTGTTGTCCCTGATTATGGTACCTACAAGAA
CACTTGTGATGGTAACACCTTTACATATGCATCTGCACTCTGGGAAATCCAGCAAGTTGTTGATGCGGATA
GCAAGATTGTTCAACTTAGTGAAATTAACATGGACAATTACCAAATTTGGCTTGGCCTCTTATTGTTACA
GCTCTAAGAGCCAACTCAGCTGTTAAACTACAGAATAATGAACTGAGTCCAGTAGCACTACGACAGATGTC
CTGTGCGGCTGGTACCACACAAACAGCTTGTACTGATGACAATGCACCTTGCCTACTATAACAATTCGAAGG
GAGGTAGGTTTGTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGATTCCCTAAGAGTGAT
GGTACAGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTTGTACAGACACACCAAAAGGGCCTAA
AGTGAAATACTTGTACTTCATCAAAGGCTTAAACAACCTAAATAGAGGTATGGTGTGCTGGGCAGTTTAGCTG
CTACAGTACGTCTTCAGGCTGGAAATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTTCTTCTGTGCT
TTTGCAGTAGACCCTGCTAAAGCATATAAGGATTACCTAGCAAGTGAGGACAACCAATCACCAACTGTGT
GAAGATGTTGTGTACACACACTGGTACAGGACAGGCAATTACTGTAAACACCAGAAGCTAACATGGACCAAG
AGTCTTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGTAGGCCACATTGACCATCCAAATCCTAAAGGATTC
TGTGACTTGAAGGTAAGTACGTCCAATACCTACCCTTGTGCTAATGACCCAGTGGGTTTTACACTTAG
AAACACAGTCTGTACCGTCTGCGGAATGTGGAAGGTTATGGCTGTAGTTGTGACCAACTCCGCGAACCTT
TGATGCAGTCTGCGGATGCATCAACGTTTTTAAACGGGTTTGCAGGTTAAGTGCAGCCCGTCTTACACCGT
GCGGCACAGGCACTAGTACTGATGTCGTCTACAGGGCTTTTGATATTTACAACGAAAAGTTGCTGGTTTT
GCAAAGTTTCTAAAACTAATTGCTGTGCTTCCAGGAGAAGGATGAGGAAGGCAATTTATTAGACTCTTA
CTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAGAGACTATTTATAACTTGGTTAAAGATT
GTCCAGCGGTTGCTGTCCATGACTTTTTCAAGTTTAGAGTAGATGGTGACATGGTACCACATATATCACGT
CAGCGTCTAACTAAATACACAATGGCTGATTTAGTCTATGCTCTACGTCATTTTGATGAGGGTAATTGTGA
TACATTAAGAAGAACTACTCGTCAACATAACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTTGGTATG
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AAGACTGTACAATTCTGCGATGCTATGCGTGATGCAGGCATTGTAGGCGTACTGACATTAGATAATCAGGA
TCTTAATGGGAAGTGGTACGATTTTCGGTGATTTTCGTACAAGTAGCACCAGGCTGCGGAGTTCCTATTGTGG
ATTCATATTACTCATTGCTGATGCCCATCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGAT
GCTGATCTCGCAAAACCACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGAAGAGAGACTTTGTCT
CTTCGACCGTTATTTTAAATATTTGGGACCAGACATACCATCCCAATTGTATTAAGTGTGTTGGATGATAGGT
GTATCCTTCATTGTGCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTACAAGTTTTGGACCACTA
GTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTGTTTCAACTGGATACCATTTTCGTGAGTTAGGAGT
CGTACATAATCAGGATGTAACTTACATAGCTCGCGTCTCAGTTTCAAGGAACCTTTTAGTGTATGCTGCTG
ATCCAGCTATGCATGCAGCTTCTGGCAATTTATTGCTAGATAAAACGCACTACATGCTTTTTCAGTAGCTGCA
CTAACAAACAATGTTGCTTTTCAAACGTGCAACCCGGTAATTTTAAATAAGACTTTTATGACTTTGCTGT
GTCTAAAGGTTTCTTTAAGGAAGGAAGTTCTGTTGAACATAAAACACTTCTTCTTTGCTCAGGATGGCAACG
CTGCTATCAGTGATTATGACTATTTATCGTTATAATCTGCCAACAAATGTGTGATATCAGACAACCTCCTATTC
GTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACGATGGTGGCTGTATTAATGCCAACCAAGTAATCGT
TAACAATCTGGATAAATCAGCTGGTTTCCCATTAAATAAATGGGGTAAGGCTAGACTTTATATGACTCAA
TGAGTTATGAGGATCAAGATGCACCTTTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATG
AATCTTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTAGTACTAT
GACAAATAGACAGTTTCATCAGAAATTTATGAAGTCAATAGCCGCCACTAGAGGAGCTACTGTGGTAATTG
GAACAAGCAAGTTTACGGTGGCTGGCATAATATGTTAAACACTGTTTACAGTGATGTAGAAACTCCACAC
CTTATGGGTTGGGATTATCCAAAATGTGACAGAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGT
TCTTGCTCGCAACATAACACTTGTGTAACCTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGC
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ATGATTCTTTCTGATGATGCCGTTGTGTGCTATAACAGTAACATATGCGGCTCAAGGTTTAGTAGCTAGCAT
TAAGAAGTTTAAAGGCAAGTTCTTTATTTATCAAAATAATGTGTTTCATGTCTGAGGCAAAATGTTGGACTGAGA
CTGACCTTACTAAAGGACCTCACGAATTTTGTCTACAGCATACAATGCTAGTTAAACAAGGAGATGATTAC
GTGTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTGTGCGATGATATTGTCAAAAC
AGATGGGTACACTTATGATTGAAAGGTTTCGTGTCTAGGCTATTGATGCTTACCCACTTACAAAACATCCTA
ATCAGGAGTATGCTGATGTCTTTCACTTGTATTTACAATACATTAGAAAGTTACATGATGAGCTTACTGGC
CACATGTTGGACATGTATTCCGTAATGCTAACTAATGATAACACCTCACGGTACTGGGAACCTGAGTTTTA
TGAGGCTATGTACACACCACATACAGTCTTGCAGGCTGTAGGTGCTTGTGATTGTGCAATTCACAGACTT

FIGURE 3D

CACTTCGTTGCGGTGCGCTGTATTAGGAGACCATTCCCTATGTTGCAAGTGCTGCTATGACCATGTCATTTCA
 ACATCACACAAATTAGTGTTGTCTGTATAATCCCTATGTTTGCAATGCCCCAGGTGTGTATGTCAGTGT
 GACACAACCTGTATCTAGGAGGTATGAGCTATTATTGCAAGTCACATAAGCCTCCCATTAGTTTTCCATTAT
 GTGCTAATGGTCAGGTTTTTGGTTTTATACAAAAACACATGTGTAGGCAGTGACAATGTCAGTACTTCAAT
 GCGATAGCAACATGTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAGAGACTCAA
 GCTTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATTTAAGCTGTCATATGGTATTGCCACTGTAC
 GCGAAGTACTCTCTGACAGAGAATTGCATCTTTTCATGGGAGGTTGGAAAACCTAGACCACCATTGAACAGA
 AACTATGCTCTTTACTGGTTACCGTGTAACATAAAAAATAGTAAAGTACAGATTGGAGAGTACACCTTTGAAAA
 AGGTGACTATGGTGATGCTGTTGTGTACAGAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTG
 TGTGACATCTCACACTGTAATGCCACTTAGTGCACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATT
 ACTGGCTTGTACCCAACACTCAACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAAGGTGCG
 CATGCAAAAGTACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTGCCATCGGACTTGCTC
 TCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATGCAGCTGTTGATGCCCTATGTGAAAAG
 GCATTAATAATTTGCCCATAGATAAATGTAGTAGAATCATACCTGCGCGTGCGCGGTAGAGTGTTTTGA
 TAAATTCAAAGTGAATTCAACACTAGAACAGTATGTTTTCTGCAGCTGTAAATGCATTGCCAGAAACAAGT
 CTGACATTGTAGTCTTTGATGAAATCTCTATGGCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTT
 CGTGCAAAACACTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCGCACATTGCTGACTAAAGG
 CACACTAGAACCAGAATATTTTAATTCAGTGTGCAGACTTATGAAAACAATAGGTCCAGACATGTTTCTTG
 GAACTTGTGCGCGTTGTCTCTGCTGAAATTGTTGACACTGTGAGTGCTTTAGTTTATGACAATAAGCTAAAA
 GCACACAAGGATAAGTCAGCTCAATGCTTCAAATGTTCTACAAAGGTGTTATTACACATGATGTTTCATC
 TGCAATCAACAGACCTCAAATAGGCGTTGTAAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTG
 TTTTATCTCACCTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTGCCTACGCAGACTGTT
 GATTCATCACAGGTTCTGAATATGACTATGTCATATTCACACAACTACTGAAACAGCACACTCTTGTA
 TGTCACCCGCTTCAATGTGGCTATCACAAGGGCAAAAATTTGGCATTGTTGTGCATAATGTCATGATAGATC
 TTTATGACAACTGAATTTACAAGTCTAGAAATACCAGCTGCAATGTGGCTACATTACAAGCAGAAAAAT
 GTAAGTGGACTTTTTAAGGACTGTAGTAAGATCATTACTGGTCTTCATCTACACAGGCACCTACACACCT
 CAGCGTTGATATAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT
 ACCGTAGACTCATCTCTATGATGGGTTTCAAATGAATTACCAAGTCAATGGTTACCCTAATATGTTTATC
 ACCCGCGAAGAAGCTATTTCGTCACGTTCTGTCGCTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAG
 AGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA
 CTGGTTATGTTGACACTGAAAAATAACACAGAATTCACCAGAGTTAATGCAAAAACCTCCACCAGGTGACCAG
 TTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAAT
 GCTCAGTGATACACTGAAAGGATTGTCAGACAGAGTCTGTTCTGCTCCTTTGGGCGCATGGCTTTGAGCTTA
 CATCAATGAAGTACTTTGTCAAGATTGGACCTGAAAGAAGTGTGTTGCTGTGTGACAAACGTGCAACTTGC
 TTTTCTACTTTCATCAGATACTTATGCCCTGCTGGAATCATTCTGTGGGTTTTGACTATGCTCTATAACCCATT
 TATGATTGATGTTTACAGAGTGGGGCTTTACGGGTAACCTTCAGAGTAACCATGACCAACATTGCCAGGTAC
 ATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTT
 AAGCGCTTGATTGGTCTGTTGAATACCTATTATAGGAGATGAAGTGAAGGTTAATCTGCTTGCAGAAA
 AGTACAACACATGGTTGTGAAGTCTGCATTGCTTGTGATAAGTTTCCAGTTCTTCATGACATTGGAAATC
 CAAAGGCTATCAAGTGTGTGCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGAC
 AAAGCTTACAAAATAGAGGAACCTCTCTATTCTTATGCTACACATCACGATAAATTCAGTATGGTGTGTTG
 TTTGTTTTTGAATTGTAACGTTGATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCT
 TGTCAAACCTGAACTTACCAGGCTGTGATGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCA
 GCTTTCGATAAAAAGTGCATTTACTAATTTAAAGCAATTGCCTTTCTTTTACTATTCTGATAGTCTTGTGA
 GTCTCATGGCAAAACAAGTAGTGTGCGGATATTGATTATGTTCCACTCAAATCTGCTACGTGTATTACACGAT
 GCAATTTAGGTGGTGCTGTTTGCAGACACCATGCAATGAGTACCGACAGTACTTGGATGCATATAATATG
 ATGATTTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATACTTATAACCTGTGGAATACATTTAC
 CAGGTTACAGAGTTTAGAAAATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGGACACGCCGGCG
 AAGCACCTGTTTTCCATCATTAATAATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTGAA
 AATAAGACAACACTTCTGTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTAACCAGTGCCAGA
 GATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTGTAATCTGGGACTACAAAAGAGAAG
 CCCAGCACATGTATCTACAATAGGTGTCTGCACATGACTGACATTGCCAAGAAACCTACTGAGAGTGCT
 TGTCTTCACTTACTGTCTTGTGTTGATGGTAGAGTGAAGGACAGGTAGACCTTTTTAGAAACCCGCTAA
 TGGTGTTTTAATAACAGAAGGTTCAAGTCAAAGGCTTAACACCTTCAAAGGGACCAGCACAAAGCTAGCGTCA
 ATGGAGTCACATTAATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACGGCATTATT
 CAACAGTTGCCGTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTAAGCCAGATCACAATGGA
 AACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGCGATATAAGCTCGAGGGCTATGCCTTCGAAC

FIGURE 3E

ACATCGTTTATGGAGATTTTCAGTCATGGACAACCTGGCGGTCTTCATTTAATGATAGGCTTAGCCAAGCGC
TCACAAGATTACCACTTAAATTAGAGGATTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAAC
AGATGCGCAAACAGGTTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGATGACTTTGTGCGAGA
TAATAAAGTCAACAAGATTTGTTCAGTGATTTCAAAAGTGGTCAAGGTTACAATTGACTATGCTGAAATTTCA
TTCATGCTTTGGTGTAAGGATGGACATGTTGAAACCTTCTACCCAAAACCTACAAGCAAGTCGAGCGTGGCA
ACCAGGTGTTGCGATGCCTAACTTGTACAAGATGCAAGAATGCTTCTTGAAAAGTGTGACCTTCAGAATT
ATGGTGAAAATGCTGTTTATACCAAAAGGAATAATGATGATGTGCGCAAAGTATACCTCAACTGTGTCAATAC
TTAAATACACTTACTTTAGCTGTACCCCTACAACATGAGAGTTATTCACCTTGGTGCTGGCTCTGATAAAGG
AGTTGCACCAGGTACAGCTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTGCGATTACAGATCTTA
ATGACTTCGTCTCCGACGCATATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGCTAATAAATGG
GACCTTATTATTAGCGATATGTATGACCCTAGGACCAAAACATGTGACAAAAGAGAATGACTCTAAAGAAGG
GTTTTTCACTTATCTGTGTGGATTTATAAAGCAAAAACCTAGCCCTGGGTGGTTCTATAGCTGTAAAGATAA
CAGAGCATTCCTTGAATGCTGACCTTTACAAGCTTATGGGCCATTTCTCATGGTGGACAGCTTTTGTTCACA
AATGTAAATGCATCATCATCGGAAGCATTTTAAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAAT
TGATGGCTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCCAGTTGTCTTCTCTATT
CACTCTTTGACATGAGCAAAATTCCTCTTAAATTAAGAGGAACCTGCTGTAATGTCTCTTAAAGGAGAATCAA
ATCAATGATATGATTTATTCTCTTCTGGAAAAAGGTAGGCTTATCATTAGAGAAAACAACAGAGTTGTGGT
TTCAAGTGATATTCTTGTTAACAACCTAAACGAACATGTTTATTCTTATTATTCTTACTCTCACTAGTG
GTAGTGACCTTGACCGGTGCACCACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCT
ATGAGGGGGGTTTACTATCCTGATGAAATTTTTAGATCAGACACTCTTATTTAACTCAGGATTTATTCTCT
TCCATTTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTGGCAACCCTGTCATACCTTTTA
AGGATGGTATTTATTTTGTCTGCCACAGAGAAATCAAATGTTGTCCGTGGTGGGTTTTTGGTTCTACCATG
AACAACAAGTCACAGTCGGTGATTATTATTAACAATTCTACTAATGTTGTTATACGAGCATGTAACCTTTGA
ATTGTGTGACAACCTTTCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTTCGATA
ATGCATTTAATTGCATTTTCGAGTACATATCTGATGCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAAT
TTTAAACACTTACGAGAGTTTGTGTTTAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAACC
TATAGATGTAGTTCTGTGATCTACCTTCTGGTTTTAAACACTTTGAAACCTATTTTAAAGTTGCCTCTTGGTA
TTAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTTACCTGCTCAAGACATTTGGGGCACGTCAGCT
GCAGCCTATTTTGTGGCTATTTAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCAC
AGATGCTGTTGATTGTTCTCAAAATCCACTTGCTGAACCTCAAATGCTCTGTTAAGAGCTTTGAGATTGACA
AAGGAATTTACCAGACCTCTAATTTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACA
AACTTGTGTCTCTTTTGGAGAGGTTTTTAATGCTACTAAATTCCTTCTGTCTATGCATGGGAGAGAAAAAA
AATTTCTAATTGTGTTGCTGATTACTCTGTGCTCTACAACCTCAACATTTTTCACCTTTAAGTGCTATG
GCGTTTCTGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGA
GATGATTTAAGACAAATAGCGCCAGGACAACTGGTGTTATTGCTGATTATAAATTATAAATTGCCAGATGA
TTTCATGGGTTGTGCTCTTGTCTTGGAACTACTAGGAACATTGATGCTACTTCAACTGGTAATTATAATTATA
AATATAGGTATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTCTCCCT
GATGGCAAACCTTGCACCCACCTGCTCTTAATTGTTATTGGCCATTAATGATTATGGTTTTTACACCAC
TACTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACTTTTAAATGCACCGGCCACGG
TTTGTGGACCAAATATCCACTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTAATGGACTCACT
GGTACTGGTGTGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTGA
TTTCACTGATTCCGTTTCGAGATCCTAAAACATCTGAAATATTAGACATTTACCTTGCCTTTTGGGGGTG
TAAGTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCACT
GATGTTTCTACAGCAATTCATGCAGATCAACTCACACAGCTTGGCGCATATATTCTACTGAGAAACAATGT
ATTCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTGCGACACTTCTTATGAGTGCGACATTCCTA
TTGGAGCTGGCATTGTGTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTG
GCTTATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATGCTATACCTACTAA
CTTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATATGT
ACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTTGCACACAACCTAAAT
CGTGCACTCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTGAAGTGTTTCGCTCAAGTCAAACAAAT
GTACAAAACCCCACTTTGAAATATTTTGGTGGTTTTAATTTTTCACAAATATTACCTGACCTCTAAAGC
CAACTAAGAGGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAG
CAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTTAC
AGTGTTGCCACCTCTGCTCAGTATGATATGATGCTGCTTACACTGCTGCTCTAGTTAGTGCTGATGCCA
CTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGTCTATGCAAATGGCATATAGGTTT
AATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAAACAAATCGCCAACCAATTTAAACAAGGC
GATTAGTCAAATTCAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACC

FIGURE 3F

AGAATGCTCAAGCATTAACACACTTGTTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTA
AATGATATCCTTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACT
TCAAAGCCTTCAAACCTATGTAACACAACAATAATCAGGGCTGCTGAAATCAGGGCTTCTGCTAATCCTTG
CTGCTACTAAAAATGCTGAGTGTGTTCTTGGACAATCAAAAAGAGTTGACTTTTGTGGAAAGGGCTACCAC
CTTATGTCTTCCCACAAGCAGCCCCGCATGGTGTGTCTTCCCTACATGTCACGTATGTGCCATCCCAGGA
GAGAACTTCACCACAGCGCCAGCAATTTGTCTATGAAGGCAAGCATACTTCCCTCGTGAAGGTGTTTTTG
TGTTTAATGGCACTTCTTGGTTTTATTACACAGAGGAACCTTCTTTCTCCACAAATAATTACTACAGACAAT
ACATTTGTCTCAGGAAATTTGTGATGTCTGTTATTGGCATCATTAACAACACAGTTTATGATCCTCTGCAACC
TGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATACATCACCAGATGTTGATCTTG
GCGACATTTTCAGGCATTAACGCTTCTGTCTGCAACATTCAAAAGAAATTGACCGCCTCAATGAGGTGCT
AAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATATTAATGGCCTTG
GTATGTTTGGCTCGGCTTCAATGCTGGACTAATTGCCATCGTCAATGTTACAATCTTGCTTTGTTGCTATGA
CTAGTTGTTGCACTTGCCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCAAGTTTGATGAGGATGACTCT
GAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAAACGAACCTTATGGATTTGTTTATGAGATTTTTT
ACTCTTGGATCAATTACTGCACAGCCAGTAAAAATTGACAATGCTTCTCCTGCAAGTACTGTTTATGCTATC
AGCAACGATACCGCTACAAGCCTCACTCCCTTTCGGATGGCTTGTTATTGGCGTTGCATTTCTTGCTGTTTT
TTCAGAGCGCTACCAAAATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCAGTTT
ATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTACATCTTTTGCTTGCTGCTGCAGGTATGGAGGC
GCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCATCAACGCATGTAGAATTATTATGAGAT
GTTGGCTTTGTTGGAAGTGCAATCCAAGAACCATTACTTTATGATGCCAACTACTTTGTTGCTGGCAC
ACACATAACTATGACTACTGTATACCATATAACAGTGTACAGATACAATTGTCTGTTACTGAAGGTGACGG
CATTTCAACACCAAACTCAAAGAAGACTACCAAAATTGGTGGTTATTCTGAGGATAGGCACCTCAGGTGTTA
AAGACTATGTCGTTGTACATGGCTATTTACCCGAAGTTTACTACCAGCTTGAGTCTACACAAATTACTACA
GACACTGGTATTGAAAATGCTACATTCTTCTATCTTTAACAAGCTTGTTAAAGACCCACCGAATGTGCAAT
ACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGCAATGGATCCAATTTATGATGAGCCGACGACGA
CTACTAGCGTGCCTTTGTAGCACAAGAAAGTGAGTACGAACCTTATGTACTCATTGCTTTGCGAAGAACAA
GGTACGTTAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTCTGCTGGTATTCTTGCTAGTCACACTAGCCAT
CCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAACGGTTT
ACGTCTACTCGCGTGTTAAAAATCTGAACCTCTTCTGAAGGAGTTCTTGATCTTCTGGTCTAAACGAACATA
CTATTATTATTTATCTGTTTGGAACTTTAACATTGCTTATCATGGCAGACAACGGTACTATTACCGTTGAG
GAGCTTAAACAACCTCCTGGAACAATGGAACCTAGTAATAGGTTTCTTATTCCTAGCCTGGATTATGTTACT
ACAATTTGCCTATTCTAATCGGAACAGGTTTTTGTACATAATAAGCTTGTTTTCTCTGCTCTTGTGGC
CAGTAACACTTGCTTGTGTTTGTGCTTGCTGCTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATT
GCAATGGCTTGATTGTAGGCTTGATGTGGCTTAGCTACTTCGTTGCTTCCTTCAGGCTGTTTGTCTCGTAC
CCGCTCAATGTGGTCATTCAACCCAGAAACAAACATTCTTCTCAATGTGCCTCTCCGGGGACAATTGTGA
CCAGACCGCTCATGGAAAGTGAACCTTGTCAATTGGTGTGATCATTCGTGGTCACTTGCGAATGGCCGGA
CACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAGATCACTGTGGCTACATCACGAACGCTTTC
TTATTACAAATTAGGAGCGTCGCAGCGTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTA
TTGGAACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAGTAAGTG
ACAACAGATGTTTCATCTTGTTGACTTCCAGGTTACAATAGCAGAGATATTGATTATCATTATGAGGACTT
TCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATTTAAGCCTCTAAT
AAGAAGAATTATTCGGAGTTAGATGATGAAGAACCTATGGAGTTAGATTATCCATAAAAACGAACATGAAAA
TTATTCTCTTCTGACATTGATTGTATTACATCTTTCGAGCTATATCACTATCAGGAGTGTGTAGAGGT
ACGACTGTACTACTAAAAGAACCCTTGCCATCAGGAACATACGAGGGCAATTACCAATTTACCCCTCTTGC
TGACAATAAATTTGCACTAACTTGCACTAGCACACACTTTGCTTTTGCTTGCTGCTGACGGTACTCGACATA
CCTATCAGCTGCGTGCAAGATCAGTTTACCAAAACTTTTCATCAGACAAGAGGAGGTTCAACAAGAGCTC
TACTCGCCACTTTTTCTCATTTGTTGCTGCTCTAGTATTTTAATACTTTGCTTACCATTAAAGAGAAAGAC
AGAATGAATGAGCTCACTTTAATTGACTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTCTTGTTTAAT
AATGCTTATTATATTTTGGTTTTTCACTCGAAATCCAGGATCTAGAAGAACCCTGTACCAAAGTCTAAACGA
ACATGAAACTTCTCATTTGTTTTGACTTGTATTTCTCTATGCAGTTGCATATGCACTGTAGTACAGCGCTGT
GCATCTAATAAACTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGGGTAATACTTATAGCACTG
CTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGATGGCACACTATGGTTCAAACATGCACACCT
AATGTTACTACTCACTGTCAAGATCCAGCTGGTGGTGGCTTATAGCTAGGTGTTGGTACCTTCATGAAGG
TACCACAACTGCTGCAATTTAGAGACGTAAGTTGTTTTTAAATAAACGAACAAATTAATAATGCTGATAAT
GGACCCCAATCAAACCAACGTAGTGCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAATAA
CCAGAATGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCCAATAATACTGCGT
CTTGGTTACAGCTCTCACTCAGCATGGCAAGGAGGAACCTAGATTCCCTCGAGGCCAGGGCGTTCCAATC

FIGURE 3G

AACACCAATAGTGGTCCAGATGACCAAATTTGGCTACTACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGA
CGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTTCTATTACCTAGGAAGCTGGCCCAGAAGCTTCACCTC
CCTACGGCGCTAACAAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCAC
ATTGGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAACCTCCTCAAGGAACAACATTGCCAAA
AGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTA
ATTCAAGAAATCAACTCCTGGCAGCAGTAGGGGAAATTTCTCCTGCTCGAATGGCTAGCGGAGGTGGTGAA
ACTGCCCTCGCGCTATTGCTGCTAGACAGATTGAACCAAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACA
ACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTG
CCACAAAACAGTACAACGTCACTCAAGCATTGTTGGGAGACGTGGTCCAGAACAACCCAAAGGAAATTTCTGGG
GACCAAGACCTAATCAGACAAGGAAGTGAATACAAACATTTGGCCGCAAATTGCACAATTTGCTCCAAGTGC
CTCTGCATTCTTTGGAATGTACGCATTGGCATGGAAGTCACACCTTCGGGAACATGGCTGACTTATCATG
GAGCCATTAAATTTGGATGACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGAC
GCATACAAAACATTTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAGACTGATGAAGCTCAGCCTTT
GCCGCAGAGACAAAAGAAGCAGCCCACTGTGACTCTTCTTCTGCGGCTGACATGGATGATTTCTCCAGAC
AACTTCAAAATTCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACTCATGATGACCACACAA
GGCAGATGGGCTATGTAAACGTTTTTCGCAATTCGGTTTACGATACATAGTCTACTCTTGTGCAGAATGAAT
TCTCGTAACTAAACAGCACAAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTA
ACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGCGAGTACGATCGAGGGTACAGT
GAATAATGCTAGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCC
CCATGTGATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 3H

CTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTTCTCTAAACGAACTTTAAAAATCTGTGT
AGCTGTGCGCTCGGCTGCATGCCTAGTGCACCTACGCAGTATAAACAATAATAAATTTTACTGTGCTTGACA
AGAAACGAGTAACCTCGTCCCTCTTCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCA
TACCTAGGTTTCGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCCTGGTGTCAACGAGAAAAAC
ACACGTCCAACCTCAGTTTGCCTGTCTTCAGGTTAGAGACGTGCTAGTGCCTGGCTTCGGGGACTCTGTGG
AAGAGGCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGTCTAGTAGAGCTGAAAAAGGC
GTACTGCCCCAGCTTGAACAGCCCTATGTGTTTCAATAACGTTCTGATGCCTTAAGCACCAATCACGGCCA
CAAGGTCGTTGAGCTGGTTGCAGAAATGGACGGCATTAGTACGGTCGTAGCGGTATAAACAATGAGGAGTAC
TCGTGCCACATGTGGGCGAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAAGGGA
GCCGGTGGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGATCCCAT
TGAAGATTATGAACAAAACCTGGAACACTAAGCATGGCAGTGGTGCACCTCCGTGAACCTACTCGTGAGCTCA
ATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGCCAGATGGGTACCCTCTTGATTGCATC
AAAGATTTTCTCGCACGCGCGGGCAAGTCAATGTGCACTCTTTCGGAACAACCTTGATTACATCGAGTCGAA
GAGAGGTGTCTACTGCTGCCGTGACCATGAGCATGAAATTCCTGGTTCACTGAGCGCTCTGATAAGAGCT
ACGAGACCCAGACACCCTTCGAAATTAAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAG
TTTGTGTTTCCCTCTTAACCTCAAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAAGACTGAGGGTTT
CATGGGGCGTATACGCTCTGTGTACCTGTTGCATCTCCACAGGAGTGTAAACAATATGCACCTTGTCTACCT
TGATGAAATGTAATCATTGCGATGAAGTTTATGGCAGACGTGCGACTTCTGAAAGCCACTTGTGAACAT
TGTGGCACTGAAAATTTAGTTATTGAAGGACCTACTACATGTGGGTACCTACCTACTAATGCTGTAGTGAA
AATGCCATGTCTGCCTGTCAAGACCCAGAGATTGGACCTGAGCATAGTGTGTCAGATTATCACAACCACT
CAAACATTGAACTCGACTCCGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTGTTTGCCTATGTT
GGCTGCTATAATAAGCGTGCCCTACTGGGTTTCTCGTGCTAGTGCTGATATTGGCTCAGGCCATACTGGCAT
TACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGAACGTGTTAACATTA
ACATTGTTGGCGATTTTCATTGAAATGAAGAGGTGGCATCATTTTGGCATCTTCTCTGCTTCTACAAGT
GCCTTTATTGACACTATAAAGAGTCTTGATTACAAGTCTTTCAAACCATTGTTGAGTCCGTGCGGTAACTA
TAAAGTTTACCAAGGGAAGCCGTAAGAGGTGCTTGGAAACATTGGACAACAGAGATCAGTTTTTAACACCAC
TGTGTGGTTTTTCCCTCACAGGCTGCTGGTGTATCAGATCAATTTTTGCGCGCACACTTGATGCAGCAAAC
CACTCAATTCCTGATTTGCAAAGAGCAGCTGTCAACATACTTGATGGTATTTCTGAACAGTCATTACGTCT
TGTCGACGCCATGGTTTATACTTCAGACCTGCTCACCACAGTGTCAATTATTATGGCATATGTAACCTGGTG
GTCTTGTACAACAGACTTCTCAGTGGTTGTCTAATCTTTTGGGCACTACTGTTGAAAAACTCAGGCCTATC
TTTGAATGGATTGAGGCGAAACCTTAGTGCAGGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATT
TCTCATTACAGGTGTTTTTGTGATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAGGATTGTG
TAAATGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAAGTCACTATCGCTGGCGCA
AAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAAAGCAAGGCACTTTACCGTCAGTGTATACG
TGGCAAGGAGCAGCTGCAACTACTCATGCCTCTTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATT
CACATGACACAGTACTTACCCTCTGAGGAGGTTGTTCTCAAGAACGGTGAACCTCGAAGCACTCGAGACGCCC
GTTGATAGCTTCACAAATGGAGCTATCGTTGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAGAT
TAAGGACAAAGAACAATACTGCGCATTTGTCTCCTGGTTTACTGGCTACAAACAATGTCTTTCGCTTAAAAG
GGGGTGACCAATTAAGGTGTAACCTTTGGAGAAGATACTGTTTGGGAAGTTCAAGGTTACAAGAATGTG
AGAATCACATTTGAGCTTGATGAACGTGTTGACAAAGTGCTTAATGAAAAGTGCTCTGTCTACACTGTTGA
ATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCAGAGGCTGTTGTGAAGACTTTACAACCAGTTT
CTGATCTCCTTACCAACATGGGTATTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGAT
GCTGGTGAAGAAAACCTTTTCATCACGTATGTATTGTCTTTTACCCTCCAGATGAGGAAGAAGAGGACGA
TGCAGAGTGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGTACAGAGGATGATTATCAAG
GTCTCCCTCTGGAATTTGGTGCCCTCAGCTGAAACAGTTTCGAGTTGAGGAAGAAGAAGAGGAAGACTGGCTG
GATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAGAACCCTACACCTGAAGAACCAGTTAATCAGTT
TACTGGTTATTTAAAACCTTACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTG
CTAATCCTATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATGGTGGTGGTGTAGCAGGTGCACCTC
AACAAGGCAACCAATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAATGGCCCTCTTACAGT
AGGAGGGTCTTGTGTTGCTTTCTGGACATAATCTTGCTAAGAAGTGCTGCTGATGTTGTTGGACCTAACCTAA
ATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCATATGAAAAATTTCAATTCACAGGACATCTTACTTGCA
CCATTGTTGTCAGCAGGCATATTTGGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGACGGTTTCG
TACACAGGTTTATATTGCAGTCAATGACAAAGCTCTTATGAGCAGGTTGTGATGATTATCTGATAACC
TGAAGCCTAGAGTGGAGCACCTAAACAAGAGGAGGACCAACACAGAGAAGATTCCAAAACCTGAGGAGAAA
TCTGTGCTACAGAAGCCTGTGATGTGAAGCCAAAAATTAAGGCCTGCATTGATGAGGTTACCACAACACT
GGAAGAACTAAGTTTCTTACCAATAAGTTACTCTTGTGCTGATATCAATGGTAAGCTTTACCATGATT
CTCAGAACATGCTTAGAGGTGAAGATATGTCTTCTTGGAGAAGGATGCACCTTACATGGTAGGTGATGTT

FIGURE 3I

ATCACTAGTGGTGATATCACTTGTGTTGTAATACCCTCCAAAAAGGCTGGTGGCACTACTGAGATGCTCTC
AAGAGCTTTGAAGAAAGTGCCAGTTGATGAGTATATAACCACGTACCCCTGGACAAGGATGTGCTGGTTATA
CACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTACCTTCAGAAGCACCT
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CAGATGCTGTTACTACATATAATGGATACCTCACTTCGTATCAAAGACATCTGAGGAGCACTTTGTAGAA
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TCTTAAGCGTGGTGACAAAATTGTGTACCACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGG
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CGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCTTATGATAATCTTAAGACAGGTGTTTCCATTCCA
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TGATGCTTATGTGACACCTTTTCAGCAACTTTTAGTGTTCCTATGGAAAACTTAAGGCACTTGTGCTA
CAGCTCACAGCGAGTTAGCAAAGGTTAGCTTTAGATGGTGTCTTTCTACATTCTGTGCTGCTGCCCCGA

FIGURE 3J

CAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTCAAACCTTTCACATCACTCTGA
CTTAGAAGTGACAGGTGACAGTTGTAACAATTTTCATGCTCACCTATAATAAGGTTGAAAACATGACGCCC
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TCTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCCGCTTATGCCACTGCCAGGAGGCCT
ATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTCGTTCTCAAAAAGTTAAAGAAATCTTTGAATGTGGCT

FIGURE 3K

AAATCTGAGTTTGACCGTGATGCTGCCATGCAACGCAAGTTGGAAAAGATGGCAGATCAGGCTATGACCCA
AATGTACAAACAGGCAAGATCTGAGGACAAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCA
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CACATGTTGGACATGTATTCCGTAATGCTAACTAATGATAACACCTCACGGTACTGGGAACCTGAGTTTAA
TGAGGCTATGTACACACCACATACAGTCTTGCAAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGACTT

FIGURE 3L

CAC TTCGTTGCGGTGCCTGTATTAGGAGACCATTCCCTATGTTGCAAGTGCTGCTATGACCATGTCATTTCA
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FIGURE 3M

ACATCGTTTATGGAGATTTTCAGTCATGGACAACCTTGGCGGTCTTCATTTAATGATAGGCTTAGCCAAGCGC
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TTAAATACACTTACTTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTTGGTGCTGGCTCTGATAAAGG
AGTTGCACCAGGTACAGCTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTGCGATTGAGATCTTA
ATGACTTCGTCTCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGCTAATAAATG
GACCTTATTATTAGCGATATGTATGACCCTAGGACCAAACATGTGACAAAAGAGAATGACTCTAAAGAAG
GTTTTTCACTTATCTGTGTGGATTTATAAAGCAAAAACCTAGCCCTGGGTGGTTCTATAGCTGTAAAGATAA
CAGAGCATTCTTGGAAATGCTGACCTTTACAAGCTTATGGGCCATTTCTCATGGTGGACAGCTTTTGTGTACA
AATGTAATGCATCATCATCGGAAGCATTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAAT
TGATGGCTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCATCTCAGTTGTCTTCTCTAT
CACTCTTTGACATGAGCAAAATTTCTCTTAATTAAGAGGAACGTGCTGAATGCTCTTAAGGAGAATCAA
ATCAATGATATGATTTATTCTCTCTGGAAGGAGTGGCTTATCATTAGAGAAAACAACAGAGGTTGTGGT
TTCAAGTGATATTCTTGTAAACAATAAACGAACATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTG
GTAGTGACCTTGACCGGTGCACCACCTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCT
ATGAGGGGGGTTTACTATCTGTGATAAATTTTAGATCAGACACTCTTATTTAACTCAGGATTTATTTCT
TCCATTTTATTTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTGGCAACCCTGTCTACACCTTTTA
AGGATGGTATTTATTTTGTGCTGCCACAGAGAAATCAAATGTTGTCCGTGGTGGGTTTTTGGTTCTACCATG
AACAACAAGTCACAGTCGGTGATTATTATTAACAATTTCTACTAATGTTGTTATACGAGCATGTAACCTTTGA
ATTGTGTGACAACCCCTTCTTTGTCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTCGATA
ATGCAATTTAATTGCACCTTCGAGTACATATCTGATGCCCTTTTCGCTTGATGTTTTCAGAAAAGTCAAGTAAT
TTTAAACACTTACGAGAGTTTGTGTTTAAAAATAAGATGGGTTTCTCTATGTTTATAAAGGCTCAACAC
TATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGAAACCTATTTTTTAAGTTGCCTCTTGGTA
TTAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCT
GCAGCCTATTTTGTGTTGGCTATTTAAAGCCAACCTACATTTATGCTCAAGTATGATGAAAATGGTACAATCAC
AGATGCTGTTGATTGTTCTCAAAATCCACTTGCTGAACCTCAAATGCTCTGTTAAGAGCTTTGAGATTGACA
AAGGAATTTACCAGACCTCTAATTTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACA
AACTTGTGTCTCTTTTGGAGAGGTTTTTAATGCTACTAAATTTCCCTTCTGTCTATGCATGGGAGAGAAAAAA
AATTTCTAATTTGTGTTGCTGATTACTCTGTGCTCTACAACCTCAACATTTTTTTTCAACCTTTAAGTGCTATG
GCGTTTCTGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGA
TTGATGATAAGACAAATAGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAAATTTGCCAGATGA
GTTCTATGGGTGTTGCTCTTGGTCTTGAATACTAGGAACATTGAGTGCTACTTCAACTGGTAAATTATAATTATA
AATATAGGTATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTTCTCCCCCT
GATGGCAAACCTTGCACCCACCTGCTCTTAATTGTTATTGGCCATTAAATGATTATGGTTTTTACACCAC
TACTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACCTTTTAAATGCACCGGCCACGG
TTTGTGGACCAAATTTATCCACTGACCTTATTAAGAACCAGTGTGTCAATTTTAAATTTTAAATGGACTCACT
GGTACTGGTGTGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCACAAATTTGGCCGTGATGTTTCTGA
TTTCACTGATTCCGTTTCGAGATCCTAAAACATCTGAAATATTAGACATTTTCACCTTGCGCTTTTGGGGGTG
TAAGTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCAC
TATGTTTTCTACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATATATTTCTACTGGAACAAATGT
ATTCAGACTCAAGCAGGTGCTTATAGGAGCTGAGCATGTGCACTCTTATGAGTGCAGAAATCTCCTAT
TTGGAGCTGGCAATTTGTGCTAGTTACCATACAGTTTCTTTTATTACGTAGTACTAGCCAAAAATCTATTTGTG
GCTTATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTAA
CTTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATATGT
ACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTTGCACACAACCTAAAT
CGTGCACCTCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTTGAAGTGTTTCGCTCAAGTCAAACAAAT
GTACAAAACCCCACTTTTGAATATTTTGGTGGTTTTTAATTTTTTCACAAATATTACCTGACCCTCTAAAGC
CAACTAAGAGGTCCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAG
CAATATGGCGAATGCCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTTAC
AGTGTTTGGCACCCTCTGCTCACTGATGATATGATGCTGCCTACACTGCTGCTCTAGTTAGTGGTACTGCCA
CTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTCAATACACTTTTGCTATGCAATGGCATATAGGTTT
AATGGCATTTGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAAACAATCGCCAACCAATTTAACAAGGC
GATTAGTCAAAATTCAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAAC

FIGURE 3N

AGAATGCTCAAGCATTAAACACACTTGTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTA
AATGATATCCTTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACT
TCAAAGCCTTCAAACCTATGTAAACACAACAACCTAATCAGGGCTGCTGAAATCAGGGCTTCTGCTAATCTTG
CTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAATCAAAAAGAGTTGACTTTTGTGGAAGGGCTACAC
CTTATGTCTTCCCACAAGCAGCCCCGCATGGTGTGTCTTCTACATGTCACGTATGTGCCATCCCAGGA
GAGGAACCTTACCACAGCGCCAGCAATTTGTCTATGAAGGCAAGCATACTTCCCTCGTGAAGGTGTTTTG
TGTTAATGGCACTTCTTGGTTTATTACACAGAGGAACCTTTTCTCCACAAATAATTACTACAGACAAT
ACATTTGTCTCAGGAAATTGTGATGTGCTTATTGGCATCATTAACAACACAGTTTATGATCCTCTGCAACC
TGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATACATCACCAGATGTTGATCTTG
GCGACATTTTACGGCATTAAACGCTTCTGTGCTCAACATTCAAAAAGAAATGACCGCCTCAATGAGGTGCT
AAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATATTAAATGGCCTTG
GTATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTTTGTGCTATGA
CTAGTTGTTGAGTTGCTTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCAAGTTTGTATGAGGATGACTCT
GAGCCAGTTCTCAAGGGTGTCAAATTACATTACATAAAACGAACCTTATGGATTTGTTTATGAGATTTTTT
ACTCTTAGATCAATTACTGCACAGCCAGTAAAAATTGACAATGCTTCTCCTGCAAGTACTGTTTCATGCTAC
AGCAACGATACCGCTACAAGCCTCACTCCCTTTCCGATGGCTTGTATTGGCGTTGCATTTCTTGCTGTTT
TTCAGAGCGCTACCAAAAATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCAGTTC
ATTTGCAATTTTACTGCTGCTATTTGTTACCATCTATTCACATCTTTTGTGCTGCTGCGTGCAGGTATGGAGGC
GCAATTTTTGTACCTCTATGCCCTGATATATTTTCTACAATGCATCAACGCATGTAGAATTATTATGAGAT
GTTGGCTTTGTTGGAAGTGCAAATCCAAGAACCATTACTTTATGATGCCAACTACTTTGTTTGTGCTGGCAC
ACACATAACTATGACTACTGTATACCATATAACAGTGTACAGATACAATGTGCTTACTGAAGGTGACGG
CATTTCAACACCAAAACTCAAAGAAGACTACCAAATTTGGTGGTTATTCTGAGGATAGGCACCTCAGGTGTTA
AAGACTATGTCGTTGTACATGGCTATTTTACCAGAAGTTTACTACCAGCTTGAGTCTACACAAATTACTACA
GACACTGGTATTGAAAATGCTACATTTCTCATCTTTAACAAGCTTGTAAAGACCCACCGAATTGTGCAAA
ACACACAATCGACGGCTCTTACGGAGTTGCTAATCAGCAATGGATCCAATTTATGATGAGCCGACGACGA
CTACTAGCGTGCCTTTGTAAGCACAAAGAAAGTGAGTACGAACCTTATGTACTCATTGCTTTGGAAGAAACA
GGTACGTTAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTGCTGGTATTCTTGCTAGTCACACTAGCCAT
CCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAACGGTTT
ACGTCTACTCGCGTGTTAAAAATCTGAACCTTCTGAAGGAGTTCTGATCTTCTGGTCTAAACGAACATA
CTATTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATGGCAGACAACGGTACTATTACCGTTGAG
GAGCTTAAACAACCTCTGGAACAATGGAACCTAGTAATAGGTTTCTTATTCCTAGCCTGGATTATGTTACT
ACAATTTGCCTATTCTAATCGGAACAGGTTTTTGTACATAATAAAGCTTGTTTTCTCTGGCTCTTGTGGC
CAGTAACACTTTGCTTGTGTTTGTGCTTGTCTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATT
GCAATAGGCTTGATTGAGGCTTGATGTGGCTTAGCTACTTCTGCTTCCCTCAGGCTGTTTGTCTCGTAC
CCGCTCAATGTGGTCATTCAACCCAGAAACAACATTCTTCTCAATGTGCCCTCTCCGGGGGACAATTGTGA
CCAGACCGCTCATGAAAAGTGAACCTGTCTATTGGTGCTGTGATCATTCGTGGTCACTTGCGAATGGCCGGA
CACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAGATCACTGTGGCTACATCACGAACGCTTTC
TTATTACAAATTAGGAGCGTCGCAGCGTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTA
TTGGAACATATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAGTAAGTG
ACAACAGATGTTTCATCTTGTGACTTCCAGGTTACAATAGCAGAGATATTGATTATCATTATGAGGACTT
TCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATTTAAGCCTCTAACT
AAGAAGAATTATTCGGAGTTAGATGATGAAGAACCTATGGAGTTAGATTATCCATAAAACGAACATGAAAA
TTATTCTCTTCTGACATTGATTGTATTACATCTTGCAGCTATATCACTATCAGGAGTGTGTTAGAGGT
ACGACTGTACTACTAAAAGAACCCTTGCCCATCAGGAACATACGAGGGCAATTACCAATTTACCCCTCTTGC
TGACAATAAATTTGCACTAACTTGCACTAGCACACACTTTGCTTTTGTGCTGTGCTGACGGTACTCGACATA
CCTATCAGCTGCGTGCAAGATCAGTTTACCAAAAACCTTTTCATCAGACAAGAGGAGGTTCAACAAGAGCTC
TACTCGCCACTTTTTCTCATTTGTGCTGCTCTAGTATTTTTAATACTTTGCTTACCATTAAAGAGAAAGAC
AGAATGAATGAGCTCACTTTAATTGACTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTTCCTTGTTTTAA
AATGCTTATTATATTTTGGTTTTCACTCGAAATCCAGGATCTAGAAGAACCCTGTACCAAAGTCTAAACGA
ACATGAAACTTCTCATTTGTTTTGACTTGTATTTCTCTATGCAGTTGCATATGCACGTGTAGTACAGCGCTGT
GCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAAGGTACAACACTAGGGGTAATACTTATAGCACTG
CTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGATGGCACACTATGGTTCAAACATGCACACCT
AATGTTACTATCAACTGTCAAGATCCAGCTGGTGGTGGCTTATAGCTAGGTGTTGGTACCTTGCATGAAGG
TCACCAAACCTGCTGCATTTAGAGACGTACTTGTGTTTTAAATAAAGCAACAAATTTAAATGTCTGATAAT
GGACCCCAATCAAACCAACGTAGTGCCCCCGCATTACATTTGGTGGACCCACAGATTTCAACTGACAATAA
CCAGAATGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCCAATAATACTGCGT
CTTGGTTTACAGCTCTCACTCAGCATGGCAAGGAGGAACCTTAGATTCCCTCGAGGCCAGGGCGTTCCAATC

FIGURE 30

AACACCAATAGTGGTCCAGATGACCAAATTGGCTACTACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGA
CGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCTTCAC TTC
CCTACGGCGCTAACAAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCAC
ATTGGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAAC TTCCTCAAGGAACAACATTGCCAAA
AGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTA
ATTCAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCCTCTGCTCGAATGGCTAGCGGAGGTGGTGAA
ACTGCCCTCGCGCTATTGCTGCTAGACAGATTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACA
ACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTG
CCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAACCCAAAGGAAATTTCTGGG
GACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAATTTGCTCCAAGTGC
CTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCTTCGGGAACATGGCTGACTTATCATG
GAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGAC
GCATACAAAACATTTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTT
GCCGCAGAGACAAAAGAAGCAGCCCACTGTGACTCTTCTTCCCTGCGGCTGACATGGATGATTTCTCCAGAC
AACTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACTCATGATGACCACACAA
GGCAGATGGGCTATGTAAACGTTTTTCGCAATTCGTTTACGATACATAGTCTACTCTTGTGCAGAAATGAAT
TCTCGTAACTAAACAGCACAAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTA
ACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGT
GAATAATGCTAGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCC
CCATGTGATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

GenBank Accession No. AY274119.2.; SEQ ID NO: 2

FIGURE 3P

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ERV-2 -----
TOR2  ACACTCATGATGACCACACAAGGCAGATGGGCATGTAAACGTTTTCGCAATTCCGTTTA
AIBV  -----

ERV-2 -----
TOR2  CGATACATAGTCTACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAAGTAGGTT
AIBV  -----

ERV-2 -----ACCCGTTACCCTAAAATTCCCTCC
TOR2  TAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTAAACATTAGGGAGGACTTG
AIBV  -----TAGTTTAGTTTAAGTTAGTTTAG
              * *   **      *

ERV-2 CCTTCTCTTCAC-----TCGCCGAGGCCACGCCGAGTAGGACCGAGGGTACAGC----
TOR2  AAAGAGCCACCACATTT--TCATCGAGGCCACGCCGAGTACGATCGAGGGTACAGT----
AIBV  AGTAGGTATAAAGATGCCAGTGCCGGGGCCACGCCGAGTACGATCGAGGGTACAGCACTA
              *          ** ***** ** *****

ERV-2 -GAGTCTTT~TAGTTTAAGGTGT~TAGATGTAAGGTACGTGGGCTTTCT--TTTGGTTTA
TOR2  -GAATAATGCTAGGGAGAGCTGCCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTA
AIBV  GGACGCCCATTAGGGGAAGA~GCTAAATTTTAGTTTAAGTTAAGTTTAA---TTGGCTAA
              **      ***   ** * * * * *      * * *   * * *

ERV-2 CTTCTTC----- GenBank: AF361253 (SEQ ID NO: 31)
TOR2  GTAGTGCTATCCCCATGTGATTTTAAATAGCTTCTTAGGAGAATGAC (SEQ ID NO: 18)
AIBV  GTATAGTTAAAATTTATAGGCTAGTATAGAGTTAGAGCA----- GenBank: NC_001451 (SEQ ID NO: 32)
              *

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Figure 4

MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSD
 TLYLTQDLFLPFYSNVTGFHTINHTFGNPVIFPKDGIYFAATEKSNVVRG
 WVFGSTMNNKSQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMGTQTHT
 MIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGLYVYKGY
 QPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSA
 AYFVGYLKPTTFMLKYDENGITITDAVDCSQNPPLAELKCSVKSFEIDKGIY
 QTSNFRVVPSPGDVVRFPNITNLCPFGEVFNATKFPVYAWERKKISNCVA
 DYSVLYNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVGDDVVRQIAPG
 QTGVIADYNYKL PDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRP
 FERDISNVFPSPDGKPCPTPALNCYWPLNDYGFYTTTGIGYQPYRVVLS
 FELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQ
 FGRDVSDFTDSDVRDPKTSEILDISPACFGGVSVITPGTNASSEVAVLYQD
 VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDI
 PIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNF
 SISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALS
 GIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFI
 EDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTD
 MIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE
 NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS
 NFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI
 RASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYV
 PSQERNFTTAPAICHEGKAYFPREGVVFVNGTSWFITQRNFFSPQIITTD
 NTFVSGNCDVVIIGIINNVTYDPLQPELDSFKEELDKYFKNHTSPDVLGD
 ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL
 GFIAGLIAIVMTILLCCMTSCCCLKGACSCGSCCKFDEDDSEPVLKGV
 KLHYT (SEQ ID NO: 33)

Figure 5

MADNGTITVEELKQLLEQWNLVIGFLFLAWIMLLQFAYSNNRNRFLYIIKL
 VFLWLLWPVTLACFVLAAYRINWVTGGIAIAMACIVGLMWLSYFVASFR
 LFARTRSMWSFNPETNILLNVPLRGITIVTRPLMESELVIGAVIIRGHLM
 AGHSLGRCDIKDLPKEITVATSRTLSTYYKLGASQRVGTDSGFAAYNRYRI
 GNYKLNTDHAGSNDNIALLV (SEQ ID NO: 34)

Figure 6

MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVS
LVKPTVYVYSRVKNLNSSEGVPDLLV (SEQ ID NO: 35)

Figure 7

MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPNNT
ASWFTALTQHGKEELRFPRGQGVPIINTNSGPDDQIGYYRRATTRVRGGDG
KMKELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTR
NPNNNAATVLQLPQGTTLPKGFYAEGSRGGSQASSRSSSRSGNSRNSTP
GSSRGNSPARMASGGGETALALLLDRLNQLESKVSQGGQQQQGQTVTKK
SAAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGTDYK
HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDN
VILLNKHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPTVTLLPAAD
MDDFSRQLQNSMSGASADSTQA (SEQ ID NO: 36)

Figure 8

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BoCov -----MSSVTPAP--VYTWTADEAIKFLKEWNFSL
OC43 -----MSSKTPAP--VYIWTADAIAKFLKEWNFSL
PHEV -----MSSPTTPVP--VISWTADEAIKFLKEWNFSL
FCV MKILLILACAVACVYGEQIRYCAMQ--ETGLSCRNGTASDCESCFCNGGDLIWHLANWNFSW
TGEV MKILLILACVIACACE--RYCAMKSDTDLSCRNSTASDCESCFCNGGDLIWHLANWNFSW
TOR2_M -----MAD--NGTTTVEELKQLEQWNLVI
ORF5 -----MAD--NGTTTVEELKQLEQWNLVI
AIBV2 -----MMEN--CTLNLEQATLLFKEYNLFI
AIBV -----MSNGTEN--CTLSTQQAELFKEYNLFI

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BoCov GIILLFITVILQFGYTSRSMFVYVIKMIILWLMWPLTIILTIFNCV--YALNN-VYLGFS
OC43 GIILLFITIILQFGYTSRSMFVYVIKMIILWLMWPLTIILTIFNCV--YALNN-VYLGFS
PHEV GIIVLFITITLQFGYTSRSMFVYVIKMIILWLMWPLTIILTIFNCV--YALNN-VYLGFS
FCV SIILLIVFITVLYQGRPQFSWFVYGIKMLIMWLLWPIVLALTIFNAYSEYVSRYVMFGFS
TGEV SIILLIVFITVLYQGRPQFSWFVYGIKMLIMWLLWPIVLALTIFNAYSEYQVSRYVMFGFS
TOR2_M GFLFLAWIMLLQFAYSNNRNFYIIKLVLWLLWPLVTLACFVLA--YRINW-VTGGIA
ORF5 GFLFLAWIMLLQFAYSNNRNFYIIKLVLWLLWPLVTLACFVLA--YRINW-VTGGIA
AIBV2 TAPLLFLTILLQYGYATRSRFIYILKMIVLWCFWPLNIAVGVIISCI--YPPNT-GGLVAA
AIBV TAPLLFLTILLQYGYATRSRFIYILKMIVLWCFWPLNIAVGVIISCI--YPPNT-GGLVAA

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BoCov IVFTIVAIIMWIVYFVNSIRLFIRTSWWSFNPETNNLMCIDMK-GRMYVRPIIEDYHTL
OC43 IVFTIVAIIMWIVYFVNSIRLFIRTSWWSFNPETNNLMCIDMK-GTMYVRPIIEDYHTL
PHEV IVFTIVAIIMWVYFVNSIRLFIRTSWWSFNPETNNLMCIDMK-GRMYVRPIIEDYHTL
FCV VAGAVVTFALWMMYFVRSIQLYRRTKSWSFNPETNAILCVNAL-GRSYVLPDGTPTGV
TGEV IAGAIVTFVLWIMYFVRSIQLYRRTKSWSFNPETKAILCVSAL-GRSYVLPLEGVPTGV
TOR2_M IAMACIVGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLR-GTIVTRPLMESELVI
ORF5 IAMACIVGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLR-GTIVTRPLMESELVI
AIBV2 IILTTFVACLSFVGYWIQSCRFLFKRCRSWWSFNPESNAVGSIILLTNGQQCNFAIESVPMVL
AIBV IILTTFVACLSFVGYWIQSCRFLFKRCRSWWSFNPESNAVGSIILLTNGQQCNFAIESVPMVL

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BoCov TVTIIRGHLYMQGIKLTGYSLSDLPAYVTVAKVSHLLTYKR---GFLDKIGDTSQFAVY
OC43 TVTIIRGHLYIQGIKLTGYSWADLPAYMTVAKVTHLCTYKR---GFLDRISDTSQFAVY
PHEV TAFTIIRGHLYIQGIKLTGYSLSDLPAYVTVAKVTHLCTYKR---GFLDRIGDTSQFAVY
FCV TLTLLSGNLYAEGFKMAGGLTIEHLPKYVMIRTPNRTIVYTLV--GKQLKATTATGWAYY
TGEV TLTLLSGNLYAEGFKIAGGMNIDNLPKYVMVALPSRTIVYTLV--GKKLKASSATGWAYY
TOR2_M GAVIIRGHLMAGHSLGR-CDIKDLPKEITVAT-SRTLSYYKL--GASQRVGTDGSGFAAY
ORF5 GAVIIRGHLMAGHSLGR-CDIKDLPKEITVAT-SRTLSYYKL--GASQRVGTDGSGFAAY
AIBV2 APIIKNGVLYCEGQWLAK-CEPDHLPKIDFVCTPDRRNIRYRMVQKYTGQDQSGNKKRVATF
AIBV SPIIKNGALYCEGQWLAK-CEPDHLPKIDFVCTPDRRNIRYRMVQKYTGQDQSGNKKRVATF

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BoCov VKSKVGNRYRLPSTQKGSGLDTALLRNNI
OC43 VKSKVGNRYRLPSTQKGSGLDTALLRNNI
PHEV VKSKVGNRYRLPSTHKGSGMDTALLRNNI
FCV VKSKAGDYSTEARTDNLSEHEKLLHVM-
TGEV VKSKAGDYSTEARTDNLSEHEKLLHVM-
TOR2_M NRYRIGNYKLNTDHAGSNDNIALLVQ--
ORF5 NRYRIGNYKLNTDHAGSNDNIALLVQ--
AIBV2 VYAKQSVDTGELESVPTGGSSLYT----
AIBV VYAKQSVDTGELGSVATGGSSLYT----

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Key	Name	Genbank	%ID	
PHEV	Porcine hemagglutinating encephalomyelitis virus	AAL80035	40.4%	(SEQ ID NO: 37)
BoCov	matrix protein [Bovine coronavirus].	NP_150082	40.0%	(SEQ ID NO: 38)
AIBV	membrane protein [Avian infectious bronchitis virus].	AAF35863	31.3%	(SEQ ID NO: 39)
TGEV	membrane protein [Transmissible gastroenteritis virus].	NP_058427	28.5%	(SEQ ID NO: 40)
FCV	membrane [feline coronavirus].	BAC01160	27.7%	(SEQ ID NO: 41)
OC43	membrane glycoprotein [Human coronavirus OC43].	AAA45462	39.1%	(SEQ ID NO: 42)
AIBV2	membrane protein [Avian infectious bronchitis virus].	AAK83027	32.0%	(SEQ ID NO: 43)
TOR2_M/ORF 5	Sars associated coronavirus M glycoprotein			(SEQ ID NO: 34)

Figure 9

```

BoCov      MSFTPGKQSS-SRASSGNRSGNGILK---WADQSDQSRNVQTRGRRRAQP--KQTATSQQP
OC43       MSFTPGKQSS-SRASSGNRSGNGILK---WADQSDQVRNVQTRGRRRAQP--KQTATSQQP
PHEV       MSFTPGKQSS-SRASSGNRSGNGILK---WADQSDQSRNVQTRGRRVQS--KQTATSQQP
MHV        MSFVPGQENAGSRSSSVNRAGNGILKKTWADQTERGPNQNRGRRNQP--KQTATTQ-P
AIBV2      -----MASGKAAGK---TDAPAPVIK----LGGPKPP--KVGSSGN--
TCV        -----MASGKATGK---TDAPAPIK----LGGPKPP--KVGSSGN--
AIBV       -----MASGKAAGK---TDAPAPVIK----LGGPKPP--KVGSSGN--
FCV        -----MATQQQVRN---WGDEPSKRR----GRSNSR--GRKNNDIP-
PTGV       -----MANQQQVRV---WGDESTKTR----GRSNSR--GRKNNNIP-
229E       -----MATVK---WADASEPQR----GRQ-----GRIPYSL--
TOR2_N     -----MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPN

```

```

BoCov      SGGNVVPYYSWFSGITQFQKGEFEFAEGQGVPIAPGVPATEAKGYWYRHNRRSFKTADG
OC43       SGGNVVPYYSWFSGITQFQKGEFEFEVEGQGPPIAPGVPATEAKGYWYRHNRRSFKTADG
PHEV       SGGTVVPYYSWFSGITQFQKGEFEFAEGQGVPIAPGVPSTEAKGYWYRHNRRSFKTADG
MHV        NSGSVVPYYSWFSGITQFQKGEFEFAEGQGVPIANGIPASEQKGYWYRHNRRSFKTADG
AIBV2      AS-----WFQAIKAKKLNTPPPKFEGSGVPDNEIKPSQQHGYWRRQAR--FKPGKG
TCV        AS-----WFQSIKAKKLNSPPKFEGSGVPDNEIKTSQQHGYWRRQAR--FKPGKG
AIBV       AS-----WFQALKAKKLNAAPKFEFGSGVPDNEIKISQQHGYWRRQAR--YKPGKG
FCV        LS-----YFNPITLDQGSKFVNLCPDRFVPKGIGNK-DQQIGYWNQAR--YRIVKG
PTGV       LS-----FFNPITLDQGSKFVNLCPDRFVPKGIGNR-DQQIGYWNQAR--YRMVKG
229E       -Y-----SPLLVDV--EQPWKVIPIRLVPIPKKDK-NKLIGYWNVQKR--FRTRKG
TOR2_N     NTAS-----WFTALTQHG--KEELRFRPGQGVPIINTNSGDDQIGYRRATRR--VRGGDG
          :               . *               . ** : * : . *

```

```

BoCov      NQRQLLPRWYFYLLGTGPHAKDQYGTIDIDGVVWASNQADVNTPADILDRDPSSDEAIP
OC43       NQRQLLPRWYFYLLGTGPHAKDQYGTIDIDGVVWASNQADVNTPADIVDRDPSSDEAIP
PHEV       NQRQLLPRWYFYLLGTGPHAKDQYGTIDIDGVVWASNQADINTPADIVDRDPSSDEAIP
MHV        QKQQLLPRWYFYLLGTGPHAGAIEYDIDIDGVVWASQQADTKTTADIVERDPSSHEAIP
AIBV2      GRKPVPDWYFYLLGTGPAADLNWGDQDGIWVVAAGADTKSRSNQGTTRDPDKFDQYPL
TCV        GRKPVPDWYFYLLGTGPAADLNWGDQDGIWVVAAGADVKSRSNQGTTRDPDKFDQYPL
AIBV       GRKPVPDWYFYLLGTGPAADLNWGDQDGIWVVAAGADVKSRSNQGTTRDPDKFDQYPL
FCV        QRVELPERWFFYLLGTGPHADAKFKIDGVVWARDGAMN-KPTSLGTRG-TNNESKPL
PTGV       QRKELPERWFFYLLGTGPHADAKFKDKLDGVVWARDGAMN-KPTTLGSRG-ANNESKAL
229E       KRVDLSPKLHFYLLGTGPHKDAKFRERVEGVVVAVDGAKT-EPTGYGVRR-KNSEPEIP
TOR2_N     KMKELSPrWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNAATVL
          :      . ** : *** :      : * : *** . *      *

```

```

BoCov      RFPFGTVLPQGYIIEGS-GRSAPNSRSTSRASSRASSA---GSRSRANSGNR---TPTSG
OC43       RFPFGTVLPQGYIIEGS-GRSAPNSRSTSRSSRASSA---GSRSRANSGNR---TPTSG
PHEV       RFPFGTVLPQGYIIEGS-GRSAPNSRSTSRAPNRAPSA---GSRSRANSGNR---TSTPG
MHV        RFAPGTVLPQGFYVEGS-GRSAPASRSGSRSQSRGP-----NNRARSSSNQR---QPAST
AIBV2      RFS DG--GPDGNFRWDF-IPLKNRGRSG-RSTAASSAA---ASRAPSRGSR---GRRSD
TCV        RFS DG--GPDGNFRWDF-IPLH-RGRSG-RSTAASSAA---SSRAPSRDGR---GRRSG
AIBV       RFS DG--GPDGNFRWDF-IPLN-RGRSG-RSTAASSAA---SSRAPSRGSR---GRLNG
FCV        KFDGK-I PPQFQLEVNR-SRNNRSRSGSQRSVSRNRS---QSRGRQQSNNQ---NTNVED
PTGV       KFDGK-VPGEFQLEVNR-SRDNSRLRSQSRSRNRS---QSRGRQQSNNKK-DDSVEQ
229E       HFNQK--LPNGVTVEE--PDSRAPSRSGSRSGRSGESKPSRNPSDRNHNSQDDIMK
TOR2_N     QLPQGTTLPGFYAEGSRGGSQASSRSSSRSGNSRSTPGSSRGNSPARMAS-GGGETA
          : :               . * * :               . *

```

```

BoCov      VTPDMADQIASLVLA KLKDAKP-----QQVTKQTAKEIRQK--IL
OC43       VTPDMADQIASLVLA KLKDATKP-----QQVTKHTAKEVRQK--IL
PHEV       VTPDMADQIASLVLA KLKDATKP-----QQVTKQTAKEVRQK--IL
MHV        VKPDMAEEIAALVLA KLKDGAP-----KQVTKQSAKEVRQK--IL
AIBV2      SGDDLIAA AKIIQDQKKGS-----RITKAKADEMAHR--RY
TCV        SEDDLIAA AKIIQDQKKGS-----RITKAKADEMAHR--RY
AIBV       AEDDLIAA AKIIQDQKKGS-----RITKAKAEEMIHR--RY
FCV        TIVAVLQKLGVTDK---QRSRSKS-----GERSQSKSRDTPK--NA
PTGV       AVLAALKKLG VYTEKQQQSRSKS-----KERSNSKIRDTPK--NE
229E       AVAAALKSLGFDKPQEKDKSAKTGTPKPSRNQSPASSQTS AKSLARSQSSETKEQKHEM
TOR2_N     LALLLLDRLNQLESKVSGKQQQGG-----QTVTKSAAEASKK--PR
          :               : :               : :

```

FIGURE 10A


```

BoCov      NKPRQKRSPNKQCT--VQQCFGKR---GPNQNFGGGEMCLKGTSDPQFPILAEALPTAGA
OC43       NKPRQKRSPNKQCT--VQQCFGKR---GPNQNFGGGEMCLKGTSDPQFPILAEALPTAGA
PHEV       NKPRQKRSPNKQCT--VQQCFGKR---GPNQNFGGGEMCLKGTSDPQFPILAEALPTAGA
MHV        NKPRQKRTPNKQCP--VQQCFGKR---GPNQNFGGSEMLKLTSDPQFPILAEALPTPSA
AIBV2      CK----RTIPPNYR--VDQVFGPRT-KGKEGNFGDDKMNEEGIKDGRVTAMLNLVPSSHA
TCV        CK----RTVPPGYK--VDQVFGPRT-KGKEGNFGDDKMNEEGIKDGRVTAMLNLVPSSHA
AIBV       CK----RTVPPGVS--IDKVFGPRT-KGKEGNFGDDKMNEEGIKDGRVTAMLNLVPSSHA
FCV        NKHTWKKTAGKGD--VTNFGYAR---SSSANFGSDLVANGNAACVFPQIAECVPSVSS
PTGV       NKHTWKKTAGKGD--VTRFYGTR---SNSANFGSDLVANGSSAKHYPQLAECVPSVSS
229E      QKPRWKRPNDVTSNVTQCFGPR---DLDNHFGSAGVVANGVKAAGYPQFAELVPSTAA
TOR2_N     QK----RTATKQYN--VTQAFGRGFEQTQGNFGDQDLIRQCTDYKHWQIAQFAPSASA
          *      :      : . : * *      . ***. :      *      . : : .*: :

```

```

BoCov      FFFGSRLLELAKVQNLSGNLDEPQKDVYELRYNGAIR-----FDSTLSGFETIMKVLNENL
OC43       FFFGSRLLELAKVQNLSGNPDEPQKDVYELRYNGAIR-----FDSTLSGFETIMKVLNENL
PHEV       FFFGSRLLELAKVQNLSGNPDEPQKDVYELRYNGAIR-----FDSTLSGFETIMKVLNQNL
MHV        FFFGSRLLELVKKN--SGGADDPKDVYELQYSGAIR-----FDSTLPGFETIMKVLNENL
AIBV2      CLFGSRVTPKLQL--DGLHLRFETTVVPCDDPQFDNYVKICDQCVDGVGTRPKDDEPKP
TCV        CLFGSRVTPKLQP--DGLHLRFETTVVPRDDPQFDNYVTICDQCVDGIGTRPKDNEPRP
AIBV       CLFGSQVTPKLQP--DGLHLTRFTTVVSRDDPQFDNYVKICDCEVDGVGTRPKDEVVRP
FCV        ILFGSQWSAEAG--DQKVTLTHNYLPLKDDAKTS-----QFLEQI
PTGV       ILFGSYWTSKEDG--DQIEVTFTHKYHLPKDDPKTG-----QFLQQI
229E      MLFDSHIVSKESG--NTVVLTFTRTVTPKDPHPLG-----KFLEEL
TOR2_N     FFGMSRIGMEVTP--SGTWLTYHGAIKLDDKDPQFK-----DN-----VILLNKHI
          :      *      .      .

```

```

BoCov      NAYQQQ--DGTMMNSPKPQRQRG---QKNGQGENDNISVAAPKSRVQNKIRELTAEDIS
OC43       NAYQQQ--DGMMNMSPKPQRQRG---HKNGQGENDNISVAVPKSRVQNKISRELTAEDIS
PHEV       NAYQHQEDGMMNISPKPQRQRG---QKNGQVENDNVSAAPKSRVQNKISRELTAEDIS
MHV        DAYQDQAGGADVSPKPKQRKRG--KQKALKGEVDNVSAAPKSSVQRNVSRRLTPEDRS
AIBV2      KSRSSSRPATRGNSPAPRQQRPK--KEKKLKKQDDEADKALTSDEERNNAQLEFYDEP-K
TCV        KSRPSSRPATRGNSPAPRQQRPK--KEKKPKKQDDEVDKALTSDEERNNAQLEFDDEP-K
AIBV       KSRSSSRPATRGTSAPKQQRPK--KEKKPKKQDDEVDKALTSDEERNNAQLEFDDEP-K
FCV        DAYKRP-----SEVAKDQRQ---RKSRSKSAERSEQEVVPDALIENYTDVFDQTQVE
PTGV       NAYARP-----SEVAKDQRQ---RKSRSKSAERSEQEVVPDALIENYTDVFDQTQVE
229E      NAFTRE-----MQQHP-----LLNPSALEFNPSQTSPTATAEVRDEVSIET-D
TOR2_N     DAYKTFPP---TEPKDKKKKTDEAQPLPQRQKKQPTVTLPLPADMDDFSRLQNSMSG
          .:      : :      . . .

```

```

BoCov      LLKKMDEP-----FTEDTSEI
OC43       LLKKMDEP-----YTEDTSEI
PHEV       LLKKMDEP-----YTEDTSEI
MHV        LLAQILDGVDGVPDGLDDSNV
AIBV2      VINWGDAA-----LGENEL--
TCV        VINWGDAA-----LGENHL--
AIBV       VINWGDAA-----LGENEL--
FCV        MIDEVTN-----
PTGV       MIDEVTN-----
229E      IIDEVN-----
TOR2_N     ASADSTQA-----

```

Key

MHV	NUCLEOCAPSID PROTEIN	Genbank	*%ID	
BoCov	nucleocapsid protein [Bovine coronavirus].	P18446	34.3%	(SEQ ID NO: 44)
AIBV	nucleocapsid protein [Avian infectious bronchitis virus].	NP_150083	34.4%	(SEQ ID NO: 45)
FCV	nucleocapsid [Feline coronavirus].	AAK27162	28.3%	(SEQ ID NO: 46)
PTGV	nucleoprotein [porcine transmissible gastroenteritis virus].	CAA74230	29.4%	(SEQ ID NO: 47)
229E	nucleocapsid protein [Human coronavirus 229E].	AAM97563	28.0%	(SEQ ID NO: 48)
OC43	NUCLEOCAPSID PROTEIN.	NP_073556	24.6%	(SEQ ID NO: 49)
PHEV	nucleocapsid protein [porcine hemagglutinating encephalomyelitis]	P33469	33.9%	(SEQ ID NO: 50)
TCV	nucleocapsid protein [turkey coronavirus].	AAL80036	33.3%	(SEQ ID NO: 51)
TOR_N	SARS associated virus nucleocapsid protein (SEQ ID NO: 35)	AAF23873	28.2%	(SEQ ID NO: 52)

FIGURE 10B

ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTG
TAGATCTGTTCTCTAAACGAACCTTTAAAATCTGTGTAGCTGTCGCTCGGC
TGCATGCCTAGTGCACCTACGCAGTATAAACAATAATAAATTTTACTGTC
GTTGACAAGAAACGAGTAACTCGTCCCTCTTCTGCAGACTGCTTACGGTT
TCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTCGTCCGGGTGT
GACCGAAAGGTAAGATGGAGAGCCTTGTCTTGGTGTCAACGAGAAAAACA
CACGTCCAACCTCAGTTTGCCTGTCTTCAGGTTAGAGACGTGCTAGTGCG
TGGCTTCGGGGACTCTGTGGAAGAGGCCCTATCGGAGGCACGTGAACACC
TCAAAAATGGCACTTGTGGTCTAGTAGAGCTGGAAAAAGGCGTACTGCCC
CAGCTTGAACAGCCCTATGTGTTTCATTAAACGTTCTGATGCCTTAAGCAC
CAATCACGGCCACAAGGTCGTTGAGCTGGTTGCAGAAATGGACGGCATTC
AGTACGGTCGTAGCGGTATAACACTGGGAGTACTCGTGCCACATGTGGGC
GAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAA
GGGAGCCGGTGGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAG
GTGACGAGCTTGGCACTGATCCCATTGAAGATTATGAACAAAACCTGGAAC
ACTAAGCATGGCAGTGGTGCACTCCGTGAACTCACTCGTGAGCTCAATGG
AGGTGCAGTCACTCGCTATGTGCAACAACATTTCTGTGGCCAGATGGGT
ACCCTCTTGATTGCATCAAAGATTTTCTCGCACGCGCGGGCAAGTCAATG
TGCACCTTTTCCGAACAACCTTGATTACATCGAGTCGAAGAGAGGTGTCTA
CTGCTGCCGTGACCATGAGCATGAAATGCTTGGTTCCTGAGCGCTCTG
ATAAGAGCTACGAGCACCAGACACCTTCGAAATTAAGAGTGCCAAGAAA
TTTGACACTTTCAAAGGGGAATGCCCAAAGTTTGTGTTTCTCTTAACTC
AAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAGACTGAGGGTT
TCATGGGGCGTATACGCTCTGTGTACCTGTTGCATCTCCACAGGAGTGT
AACAATATGCACCTTGCTACCTTGATGAAATGTAATCATTGCGATGAAGT
TTCATGGCAGACGTGCGACTTTCTGAAAGCCACTTGTGAACATTGTGGCA
CTGAAAATTTAGTTATTGAAGGACCTACTACATGTGGGTACCTACCTACT
AATGCTGTAGTGAAGATGCCATGTCTGCTGTCAAGACCCAGAGATTGG
ACCTGAGCATAGTGTGTCAGATTATCACAACCACTCAAACATTGAAACTC
GACTCCGCAAGGGAGGTAGGACTAGATGTTTGGAGGCTGTGTGTTTGCC
TATGTTGGCTGCTATAATAAGCGTGCCTACTGGGTTCCCTCGTGCTAGTGC
TGATATTGGCTCAGGCCATACTGGCATTACTGGTGACAATGTGGAGACCT
TGAATGAGGATCTCCTTGAGATACTGAGTCGTGAACGTGTTAACATTAAAC
ATTGTTGGCGATTTTCAATTTGAATGAAGAGGTTGCCATCATTTTGGCATC
TTTCTCTGCTTCTACAAGTGCCCTTTATTGACACTATAAAGAGTCTTGATT
ACAAGTCTTTCAAACCATTTGTTGAGTCCTGCGGTAACATAAAGTTACC
AAGGGAAAGCCCGTAAAAGGTGCTTGGAACATTGGACAACAGAGATCAGT
TTTAACACCACTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTATCAGAT
CAATTTTTCGCGCACACTTGATGCAGCAAACCACTCAATTCCTGATTTG
CAAAGAGCAGCTGTACCATACTTGATGGTATTTCTGAACAGTCATTACG
TCTTGTGTCAGGCCATGGTTTATACTTCAGACCTGCTCACCAACAGTGTCA
TTATTATGGCATATGTAACCTGGTGGTCTTGTACAACAGACTTCTCAGTGG
TTGTCTAATCTTTTGGGCACTACTGTTGAAAACTCAGGCCTATCTTTGA
ATGGATTGAGGCGAACTTAGTGACAGGAGTTGAATTTCTCAAGGATGCTT
GGGAGATTCTCAAATTTCTCATTACAGGTGTTTTTGGACATCGTCAAGGGT
CAAATACAGGTTGCTTCAGATAACATCAAGGATTGTGTAAAATGCTTCAT
TGATGTTGTAAACAAGGCACTCGAAATGTGCATTGATCAAGTCACTATCG
CTGGCGCAAAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAA
AGCAAGGGACTTTACCGTCAGTGTATACGTGGCAAGGAGCAGCTGCAACT
ACTCATGCCCTCTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATT
CACATGACACAGTACTTACCTCTGAGGAGGTGTTCTCAAGAACGGTGAA
CTCGAAGCACTCGAGACGCCCCGTTGATAGCTTCACAAATGGAGCTATCGT
TGGCACACCAGTCTGTGTAATGGCCTCATGCTCTTAGAGATTAAAGGACA
AAGAACAATACTGCGCATTTGTCTCCTGGTTTACTGGCTACAAACAATGTC
TTTCGCTTAAAAGGGGGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGA
TACTGTTTGGGAAGTTCAAGGTTACAAGAATGTGAGAATCACATTTGAGC
TTGATGAACGTGTTGACAAAGTGCTTAATGAAAAGTGCTCTGTCTACACT

FIGURE 11A

GTGGAATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCAGAGGC
TGTTGTGAAGACTTTACAACCACTTCTGATCTCCTTACCAACATGGGTA
TTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGATGCT
GGTGAAGAAAACTTTTCATCACGTATGTATTGTTCCCTTTTACCCTCCAGA
TGAGGAAGAAGAGGACGATGCAGAGTGTGAGGAAGAAGAAATTGATGAAA
CCTGTGAACATGAGTACGGTACAGAGGATGATTATCAAGGTCTCCCTCTG
GAATTTGGTGCCTCAGCTGAAACAGTTTCGAGTTGAGGAAGAAGAAGAGGA
AGACTGGCTGGATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAG
AACCTACACCTGAAGAACCAGTTAATCAGTTTACTGGTTATTTAAACTT
ACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAG
TGCTAATCCTATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATG
GTGGTGGTGTAGCAGGTGCACCTCAACAAGGCAACCAATGGTGCCATGCAA
AAGGAGAGTGATGATTACATTAAGCTAAATGGCCCTCTTACAGTAGGAGG
GTCTTGTGTTGCTTTCTGGACATAATCTTGCTAAGAAGTGTCTGCATGTTG
TTGGACCCTAACCTAAATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCA
TATGAAAATTTCAATTACAGGACATCTTACTTGCAACATTGTTGTCAGC
AGGCATATTTGGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGA
CGGTTTCGTACACAGGTTTATATGTCAGTCAATGACAAAGCTCTTTATGAG
CAGGTTGTCATGGATTATCTTGATAACCTGAAGCCTAGAGTGGAAGCACC
TAAACAAGAGGAGCCACCAAACACAGAAGATTCCAAAACCTGAGGAGAAAT
CTGTCGTACAGAAGCCTGTGCGATGTGAAGCCAAAATTAAGGCCTGCATT
GATGAGGTACCACAACACTGGAAGAACTAAGTTTCTTACCAATAAGTT
ACTCTTGTGTTGCTGATATCAATGGTAAGCTTTACCATGATTCTCAGAAC
TGCTTAGAGGTGAAGATATGTCTTTCCTTGAGAAGGATGCACCTTACATG
GTAGGTGATGTTATACACTAGTGGTGATATCACTTGTGTTGTAATACCTC
CAAAAAGGCTGGTGGCACTACTGAGATGCTCTCAAGAGCTTTGAAGAAAG
TGCCAGTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGT
TATACACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATT
TTATGTACTACCTTCAGAAGCACCTAATGCTAAGGAAGAGATTCTAGGAA
CTGTATCCTGGAATTTGAGAGAAATGCTTGCTCATGCTGAAGAGACAAGA
AAATTAATGCCTATATGCATGGATGTTAGAGCCATAATGGCAACCATCCA
ACGTAAGTATAAAGGAATTAATAATCAAGAGGGCATCGTTGACTATGGTG
TCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCTTCTATTATTACG
AAGCTGAACCTCTCTAAATGAGCCGCTTGTACAAATGCCAATTGGTTATGT
GACACATGGTTTTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTA
AAGCTCCTGCCGTAGTGTGAGTATCATCACCAGATGCTGTTACTACATAT
AATGGATACCTCACTTCGTATCAAGACATCTGAGGAGCACTTTGTAGA
AACAGTTTCTTTGGCTGGCTCTTACAGAGATTGGTCCCTATTTCAGGACAGC
GTACAGAGTTAGGTGTTGAATTTCTTAAGCGTGGTGACAAAATTGTGTAC
CACACTCTGGAGAGCCCCGTGAGTTTCATCTTGACGGTGAGGTTCTTTC
ACTTGACAACTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAA
AAGTGTTCACAACCTGTGGACAACACTAATCTCCACACACAGCTTGTGGAT
ATGTCTATGACATATGGACAGCAGTCTTGGTCCAACATACTTGATGGTGC
TGATGTTACAAAATTAACCTCATGTAAATCATGAGGGTAAGACTTTCT
TTGTACTACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTAC
CATACTCTTGATGAGAGTTTTCTTGGTAGGTACATGTCTGCTTTAAACCA
CACAAAGAAATGGAAATTTCTCAAGTTGGTGGTTTTAACTTCAATTAAAT
GGGCTGATAACAATTGTTATTTGTCTAGTGTTTTATTAGCACTTCAACAG
CTTGAAAGTCAAATTCATGCACCAGCACTTCAAGAGGCTTATTATAGAGC
CCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTCGCTTACAGTA
ATAAACTGTTGGCGAGCTTGGTGATGTCAGAGAACTATGACCCATCTT
CTACAGCATGCTAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTG
TAAACATTTGGTTCAGAAAACCTACTACCTTAACGGGTGTAGAAGCTGTGA
TGTATATGGGTACTCTATCTTATGATAATCTTAAGACAGGTGTTTCCATT
CCATGTGTGTGTGGTGTGATGCTACACAATATCTAGTACAACAAGAGTC
TTCTTTTGTATGATGTCTGCACCACCTGCTGAGTATAAATTACAGCAAG
GTACATTCTTATGTGCAATGAGTACACTGGTAACCTATCAGTGTGGTCAT

FIGURE 11B

TACACTCATATAACTGCTAAGGAGACCCTCTATCGTATTGACGGAGCTCA
CCTTACAAAGATGTCAGAGTACAAAGGACCAGTGACTGATGTTTTCTACA
AGGAAACATCTTACACTACAACCATCAAGCCTGTGTCGTATAAACTCGAT
GGAGTTACTTACACAGAGATTGAACCAAAATTTGGATGGGTATTATAAAAA
GGATAATGCTTACTATACAGAGCAGCCTATAGACCTTGTACCAACTCAAC
CATTACCAAATGCGAGTTTTGATAATTTCAAACCTCACATGTTCTAACACA
AAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTC
ACGAGAGCTATCTGTACATTCTTCCCAGACTTGAATGGCGATGTAGTGG
CTATTGACTATAGACACTATTACAGCGAGTTTCAAGAAAGGTGCTAAATTA
CTGCATAAGCCAATTGTTTGGCACATTAACCAGGCTACAACCAAGACAAC
GTTCAAACCAAACACTTGGTGTATTACGTTGTCTTTGGAGTACAAAGCCAG
TAGATACCTCAAATTCATTTGAAGTCTTGGCAGTAGAAGACACACAAGGA
ATGGACAATCTTGCTTGTGAAAGTCAACAACCCACCTCTGAAGAAGTAGT
GGAAAATCCTACCATAACAGAAGGAAGTCATAGAGTGTGACGTGAAAACCTA
CCGAAGTTGTAGGCAATGTCATACTTAAACCATCAGATGAAGGTGTTAA
GTAACACAAGAGTTAGGTCATGAGGATCTTATGGCTGCTTATGTGGAAAA
CACAAGCATTACCATTAAAGAAACCTAATGAGCTTTCACTAGCCTTAGGTT
TAAAAACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGG
AGTAAAATTTTGGCTTATGTCAAACCATTCCTTAGGACAAGCAGCAATTAC
AACATCAAATTCGCTAAGAGATTAGCACAAACGTGTGTTTAAACAATTATA
TGCCTTATGTGTTTACATTATTGTTCCAATTGTGTACTTTTACTAAAAGT
ACCAATTC TAGAATTAGAGCTTCACTACCTACAACCTATTGCTAAAAATAG
TGTTAAGAGTGTTGCTAAATTAATGTTTGGATGCCGGCATTAAATTATGTGA
AGTCACCCAAATTTTCTAAATTTGTTTACAATCGCTATGTGGCTATTGTTG
TTAAGTATTGTGCTTAGGTTCTCTAATCTGTGTAAGTGTGCTTTTGGTGT
ACTCTTATCTAATTTTGGTGTCTCTTCTTATTGTAATGGCGTTAGAGAAT
TGTATCTTAATTCGTCTAACGTTACTACTATGGATTTCTGTGAAGGTTCT
TTTCCTTGCAGCATTTGTTTAAAGTGGATTAGACTCCCTTGATTCTTATCC
AGCTCTTGAACCATTCAGGTGACGATTTTCATCGTACAAGCTAGACTTGA
CAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCATATATGTTGTTTACA
AAATTCCTTTTATTTATTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGG
CTATTTTGCTAGTCATTTTCATCAGCAATTCCTTGGCTCATGTGGTTTATCA
TTAGTATTGTACAAATGGCACCCGTTTCTGCAATGGTTAGGATGTACATC
TTCTTTGCTTCTTCTACTACATATGGAAGAGCTATGTTTATATCATGGA
TGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGCAATCGTGCCA
CACGCGTTGAGTGTACAACCTATTGTTAATGGCATGAAGAGATCTTCTAT
GTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAATTGGAATTG
TCTCAATTGTGACACATTTTGCACCTGGTAGTACATTATTAGTGATGAAG
TTGCTCGTGATTTGTCACTCCAGTTTAAAAGACCAATCAACCCTACTGAC
CAGTCATCGTATATTGTTGATAGTGTGCTGTGAAAAATGGCGCGCTTCA
CCTCTACTTTTGACAAGGCTGGTCAAAAGACCTATGAGAGACATCCGCTCT
CCCATTTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCA
CTGCCTATTAAATGTCATAGTTTTTGATGGCAAGTCCAAATGCGACGAGTC
TGCTTCTAAGTCTGCTTCTGTGTACTACAGTCAGCTGATGTGCCAACCTA
TTCTGTTGCTTGACCAAGCTCTTGTATCAGACGTTGGAGATAGTACTGAA
GTTTCCGTTAAGATGTTTGTATGCTTATGTGACACCTTTTCAGCAACTTT
TAGTGTTCCTATGGA AAAA ACTTAAGGCACTTGTTGCTACAGCTCACAGCG
AGTTAGCAAAGGGTG TAGCTTTAGATGGTGTCTTTCTACATTCTGTGTCA
GCTGCCCCGACAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTAT
TGAATGTCTCAAACCTTTCACATCACTCTGACTTAGAAGTGACAGGTGACA
GTTGTAACAATTTTCATGCTCACCCTATAATAAGGTTGAAAACATGACGCCC
AGAGATCTTGGCGCATGTATTGACTGTAATGCAAGGCATATCAATGCCCA
AGTAGCAAAAAGTCACAATGTTTCACTCATCTGGAATGTAAAAGACTACA
TGTCTTTATCTGAACAGCTGCGTAAACAAATTCGTAGTGCTGCCAAGAAG
AACACATACTTTTAGACTAACTTGTGCTACAACCTAGACAGGTGTCAA
TGTACATAACTACTAAAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTT
GTTTTAAACTTATGCTTAAGGCCACATTATTGTGCGTTCTTGCTGCATTG

FIGURE 11C

GTTTGTATATATCGTTATGCCAGTACATACATTGTCAATCCATGATGGTTA
CACAAATGAAATCATTTGGTTACAAAGCCATTCAGGATGGTGTCACTCGTG
ACATCATTTTCTACTGATGATTGTTTTGCAAAATAACATGCTGGTTTTGAC
GCATGGTTTTAGCCAGCGTGGTGGTTCATACAAAAATGACAAAAGCTGCCC
TGATAGTACTGCTATCATTACAAGAGAGATTGGTTTTCATAGTGCCTGGCT
TACCGGGTACTGTGCTGAGAGCAATCAATGGTGACTTCTTGCAATTTTCTA
CCTCGTGTTTTTTAGTGCTGTTGGCAACATTTGCTACACACCTTCCAAACT
CATTGAGTATAGTGATTTTGCTACCTCTGCTTGCGTTCCTTGCTGCTGAGT
GTACAATTTTTAAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGAC
ACTAATTTGCTAGAGGGTTCTATTTCTTATAGTGAGCTTCGTCCAGACAC
TCGTTATGTGCTTATGGATGGTTCCATCATAACAGTTTCCTAACACTTACC
TGGAGGGTCTCTGTTAGAGTAGTAACAACCTTTTGATGCTGAGTACTGTAGA
CATGGTACATGCGAAAGGTCAGAAGTAGGTATTTGCCCTATCTACCAGTGG
TAGATGGGTTCCTTAATAATGAGCATTACAGAGCTCTATCAGGAGTTTTCT
GTGGTGTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTGCTG
CAACCTGTGGGTGCTTTTAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTAT
TATTGCCATATTGGTGACTTGTGCTGCCACTACTTTTATGAAATTCAGAC
GTGTTTTTGGTGAGTACAACCATGTTGTTGCTGCTAATGCACTTTTGTTT
TTGATGTCTTTCACTATACTCTGTCTGGTACCAGCTTACAGCTTTCTGCC
GGGAGTCTACTCAGTCTTTTACTTGTACTTGACATTCTATTTACCAATG
ATGTTTCATTCTTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATT
GTGCCTTTTTGGATAACAGCAATCTATGTATTCTGTATTTCTCTGAAGCA
CTGCCATTGGTTCCTTAACAACATCTTAGGAAAAGAGTCATGTTTAATG
GAGTTACATTTAGTACCTTCGAGGAGGCTGCTTTGTGTACCTTTTTGCTC
AACAAGGAAATGTACCTAAAATTGCGTAGCGAGACACTGTTGCCACTTAC
ACAGTATAACAGGTCTTGCTCTATATAACAAGTACAAGTATTTCAAGTG
GAGCCTTAGATACTACCAGCTATCGTGAAAGCAGCTTGCTGCCACTTAGCA
AAGGCTCTAAATGACTTTAGCAACTCAGGTGCTGATGTTCTCTACCAACC
ACCACAGACATCAATCACTTCTGCTGTTCTGCAGAGTGGTTTTAGGAAA
TGGCATTCCCCTCAGGCAAAGTTGAAGGGTGCATGGTACAAGTAACCTGT
GGAAC TACAACCTCTAATGGATTGTGGTTGGATGACACAGTATACTGTCC
AAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCTAACTATGAAG
ATCTGCTCATTCGCAAATCCAACCATAGCTTTCTTGTTCAGGCTGGCAAT
GTTCAACTTCGTGTTATTGGCCATTCTATGCAAAATTGTCTGCTTAGGCT
TAAAGTTGATATCTTCTAACCCTAAGACACCCAAAGTATAAATTTGTCCGTA
TCCAACCTGGTCAAACATTTTCAAGTTCTAGCATGCTACAATGGTTACCA
TCTGGTGTTTATCAGTGTGCCATGAGACCTAATCATACCATTAAGGTTT
TTTCTTAATGGATCATGTGGTAGTGTGGTTTTAACATTGATTATGATT
GCGTGTCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACAC
GCTGGTACTGACTTAGAAGGTAAATCTATGGTCCATTTGTTGACAGACA
AACTGCACAGGCTGCAGGTACAGACACAACCATAACATTAATGTTTTGG
CATGGCTGTATGCTGCTGTTATCAATGGTGATAGGTGGTTTTCTTAATAGA
TTCACCACTACTTTGAATGACTTTAACCTTGTGGCAATGAAGTACAAC TA
TGAACCTTTGACACAAAGATCATGTTGACATATTGGGACCTCTTTCTGCTC
AAACAGGAATTGCCGCTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTG
CAGAAATGGTATGAATGGTCGTACTATCCTTGGTAGCACTATTTTAGAAGA
TGAGTTTACACCATTTGATGTTGTTAGACAATGCTCTGGTGTACCTTCC
AAGGTAAGTTCAAGAAAATTGTTAAGGGCACTCATATTGGATGCTTTTA
ACTTTCTTGACATCACTATTGATTCTTGTTCAAAGTACACAGTGGTCACT
GTTTTTCTTTGTTTACGAGAATGCTTTCTTGCCATTTACTCTTGGTATTA
TGGCAATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAGCACGCATTC
TTGTGCTTGTTCCTGTTACCTTCTCTTGCAACAGTTGCTTACTTTAATAT
GGCTACATGCCCTGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAAT
TGGCTGACACTAGCTTGTCTGGTTATAGGCTTAAGGATTGTGTTATGTAT
GCTTCAGCTTTAGTTTTGCTTATTCTCATGACAGCTCGCACTGTTTATGA
TGATGCTGCTAGACGTGTTTGGACACTGATGAATGTCATTACACTTGTTT
ACAAAGTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGGCC

FIGURE 11D

TTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTCTGTTACGACTATCAT
GTTTTTAGCTAGAGCTATAGTGTGTTGTGTGTTGAGTATTACCCATTGT
TATTTATTACTGGCAACACCTTACAGTGATCATGCTTGTGTTATTGTTTC
TTAGGCTATTGTTGCTGCTGCTACTTTGGCCTTTTCTGTTTACTCAACCG
TTACTTCAGGCTTACTCTTGGTGTGTTATGACTACTTGGTCTCTACACAAG
AATTTAGGTATATGAACCTCCAGGGGCTTTTGCCCTCCTAAGAGTAGTATT
GATGCTTTCAAGCTTAACATTAAGTTGTTGGGTATTGGAGGTAAACCATG
TATCAAGGTTGCTACTGTACAGTCTAAAAATGCTCTGACGTAAAGTGCACAT
CTGTGGTACTGCTCTCGGTTCTTCAACAACCTTAGAGTAGAGTCATCTTCT
AAATTGTGGGCACAATGTGTACAACCTCCACAATGATATTCTTCTTGCAA
AGACACAACCTGAAGCTTTTCGAGAAGATGGTTCCTCTTTTGTCTGTTTTGC
TATCCATGCAGGGTGTCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTC
GATAACCGTGCTACTCTTCAGGCTATTGCTTCAGAAATTTAGTTCTTTACC
ATCATATGCCGCTTATGCCACTGCCAGGAGGCCATGAGCAGGCTGTAG
CTAATGGTGATTCTGAAGTCGTTCTCAAAAAGTTAAAGAAATCTTTGAAT
GTGGCTAAATCTGAGTTTGACCGTGATGCTGCCATGCAACGCAAGTTGGA
AAAGATGGCAGATCAGGCTATGACCCAAATGTACAAACAGGCAAGATCTG
AGGACAAGAGGGCAAAAGTAACCTAGTGCTATGCAAACAATGCTCTTCACT
ATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGC
GCGTGATGGTTGTGTTCCACTCAACATCATACCATTGACTACAGCAGCCA
AACTCATGGTTGTTGTCCCTGATTATGGTACCCTACAAGAACACTTGTGAT
GGTAACACCTTTACATATGCATCTGCACTCTGGGAAATCCAGCAAGTTGT
TGATGCGGATAGCAAGATTGTTCAACTTAGTGAAATTAACATGGACAATT
CACCAAATTTGGCTTGGCCTCTTATTGTTACAGCTCTAAGAGCCAACCTCA
GCTGTTAAACTACAGAATAATGAACCTGAGTCCAGTAGCACTACGACAGAT
GTCCGTGTGCGGCTGGTACCACACAAACAGCTTGTACTGATGACAATGCAC
TTGCCCTACTATAACAATTCGAAGGGAGGTAGGTTTGTGCTGGCATTACTA
TCAGACCACCAAGATCTCAAATGGGCTAGATTCCCTAAGAGTGATGGTAC
AGGTACAATTTACACAGAAGCTGGAACCACTTGTAGGTTTGTACAGACA
CACCAAAGGGCCTAAAGTGAAATACTTGTACTTCATCAAAGGCTTAAAC
AACCATAATAGAGGTATGGTGCTGGGCAGTTTAGCTGCTACAGTACGTCT
TCAGGCTGGAATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTCCCT
TCTGTGCTTTTGCAGTAGACCCTGCTAAAGCATATAAGGATTACCTAGCA
AGTGGAGGACAACCAATCACCACCTGTGTGAAGATGTTGTGTACACACAC
TGGTACAGGACAGGCAATTACTGTAAACACCAGAAGCTAACATGGACCAAG
AGTCCCTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGAC
CATCCAAATCCTAAAGGATTCTGTGACTTGAAAGGTAAGTACGTCCAAAT
ACCTACCACCTGTGCTAATGACCCAGTGGGTTTTACACTTAGAAACACAG
TCTGTACCGTCTGCGGAATGTGGAAGGTTATGGCTGTAGTTGTGACCAA
CTCCGCGAACCCTTGATGCAGTCTGCGGATGCATCAACGTTTTTAAACGG
GTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGTGCGGCACAGGCACTAG
TACTGATGTCGCTACAGGGCTTTTGATATTTACAACGAAAAAGTTGCTG
GTTTTGCAAAGTTCTAAAACTAATTGCTGTCTGCTTCCAGGAGAAGGAT
GAGGAAGGCAATTTATTAGACTCTTACTTTGTAGTTAAGAGGCATACTAT
GTCTAACTACCAACATGAAGAGACTATTTATAACTTGGTTAAAGATTGTC
CAGCGGTTGCTGTCCATGACTTTTTCAAGTTTAGAGTAGATGGTGACATG
GTACCACATATATCACGTCAGCGTCTAACTAAATACACAATGGCTGATTT
AGTCTATGCTCTACGTCATTTTGTATGAGGGTAATTGTGATACATTAAAG
AAATACTCGTCACATACAATTGCTGTGATGATGATTATTTCAATAAGAAG
GATTGGTATGACTTCGTAGAGAATCCTGACATCTTACGCGTATATGCTAA
CTTAGGTGAGCGGTACGCCAATCATTATTAAGACTGTACAATTCTGCG
ATGCTATGCGTGATGCAGGCATTGTAGGCGTACTGACATTAGATAATCAG
GATCTTAATGGGAACCTGGTACGATTTTCGGTGATTTTCGTACAAGTAGCACC
AGGCTGCGGAGTTCCATTGTGGATTTCATATTACTCATTTGCTGATGCCCA
TCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGATGCTGAT
CTCGCAAAACCACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGA
AGAGAGACTTTGTCTCTTCGACCGTTATTTTAAATATTGGGACCAGACAT

FIGURE 11E

ACCATCCCAATTGTATTAACTGTTTGGATGATAGGTGTATCCTTCATTGT
GCAAACCTTTAATGTGTTATTTTCTACTGTGTTTCCACCTACAAGTTTTGG
ACCACTAGTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTGTTTCAA
CTGGATACCATTTTCGTGAGTTAGGAGTCGTACATAATCAGGATGTAAAC
TTACATAGCTCGCGTCTCAGTTTCAAGGAACTTTATGTATGCTGCTGA
TCCAGCTATGCATGCAGCTTCTGGCAATTTATTGCTAGATAAACGCACTA
CATGCTTTTTCAGTAGCTGCACTAACAAACAATGTTGCTTTTCAAACGTGTC
AAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTGTGTCTAAAGG
TTTCTTTAAGGAAGGAAGTTCTGTTGAACATAAACACTTCTTCTTTGCTC
AGGATGGCAACGCTGCTATCAGTGATTATGACTATTATCGTTATAATCTG
CCAACAATGTGTGATATCAGACAACCTCCTATTTCGTAGTTGAAGTTGTTGA
TAAATACCTTTGATTGTTACGATGGTGGCTGTATTAATGCCAACCAAGTAA
TCGTTAACAATCTGGATAAATCAGCTGGTTTCCCATTTAATAAATGGGGT
AAGGCTAGACTTTTATTATGACTCAATGAGTTATGAGGATCAAGATGCACT
TTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATGAATC
TTAAGTATGCCATTAGTGC AAAAG AATAGAGCTCGCACCGTAGCTGGTGTC
TCTATCTGTAGTACTATGACAAAATAGACAGTTTTCATCAGAAATTATTGAA
GTCAATAGCCGCCACTAGAGGAGCTACTGTGGTAATTGGAACAAGCAAGT
TTTACGGTGGCTGGCATAATATGTTAAAAACTGTTTACAGTGATGTAGAA
ACTCCACACCTTATGGGTTGGGATTATCCAAAATGTGACAGAGCCATGCC
TAACATGCTTAGGATAATGGCCTCTCTTGTCTTGTCTCGCAAACATAACA
CTTGCTGTAACCTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCG
CAAGTATTAAGTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACC
AGGTGGAACATCATCCGGTGATGCTACAACCTGCTTATGCTAATAGTGTCT
TTAACATTTGTCAAGCTGTTACAGCCAATGTAAATGCACCTTCTTTCAACT
GATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTACAACACAGGCT
CTATGAGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATG
AGTTTTACGCTTACCTGCGTAAACATTTCTCCATGATGATTCTTTCTGAT
GATGCCGTTGTGTGCTATAACAGTAACCTATGCGGCTCAAGGTTTAGTAGC
TAGCATTAAGAACTTTAAGGCAGTTCTTTATTATCAAAATAATGTGTTCA
TGCTTGAGGCAAAATGTTGGACTGAGACTGACCTTACTAAAGGACCTCAC
GAATTTTGTCTCACAGCATACAATGCTAGTTAAACAAGGAGATGATTACGT
GTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTG
TCGATGATATTGTCAAAACAGATGGTACACTTATGATTGAAAGGTTTCGTG
TCACTGGCTATTGATGCTTACCCACTTACAAAACATCCTAATCAGGAGTA
TGCTGATGTCTTTCACTTGTATTTACAATACATTAGAAAGTTACATGATG
AGCTTACTGGCCACATGTTGGACATGTATTCGGTAATGCTAACTAATGAT
AACACCTCACGGTACTGGGAACCTGAGTTTATGAGGCTATGTACACACC
ACATACAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGA
CTTCACTTCGTTGCGGTGCCTGTATTAGGAGACCATTCCTATGTTGCAAG
TGCTGCTATGACCATGTCAATTTCAACATCACACAAATTAGTGTTGTCTGT
TAATCCCCTATGTTTGCAATGCCCCAGGTTGTGATGTCACTGATGTGACAC
AACTGTATCTAGGAGGTATGAGCTATTATTGCAAGTCACATAAGCCTCCC
ATTAGTTTTCCATTATGTGCTAATGGTCAGGTTTTTGGTTTTATACAAAAA
CACATGTGTAGGCAGTGACAATGTCACTGACTTCAATGCGATAGCAACAT
GTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAG
AGACTCAAGCTTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATT
TAAGCTGTATATGGTATTGCCACTGTACGCGAAGTACTCTCTGACAGAG
AATTGCATCTTTTCATGGGAGGTTGGAAAACCTAGACCACCATTGAACAGA
AACTATGTCTTTTACTGGTTACCGTGTAACCTAAAAATAGTAAAGTACAGAT
TGGAGAGTACACCTTTGAAAAAGGTGACTATGGTGATGCTGTTGTGTACA
GAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTGTGTTGACA
TCTCACACTGTAGTACCACTTAGTACGACCTACTCTAGTGCCACAAGAGCA
CTATGTGAGAATTACTGGCTTGTAACCAACACTCAACATCTCAGATGAGT
TTTCTAGCAATGTTGCAAATTATCAAAAAGTCGGCATGCAAAAGTACTCT
ACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTGCCATCGGACT
TGCTCTCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATG

FIGURE 11F

CAGCTGTTGATGCCCTATGTGAAAAGGCATTAAAATATTTGCCCATAGAT
AAATGTAGTAGAATCATACCTGCGCGTGCGCGCTAGAGTGTTTTGATAA
ATTCAAAAGTGAATTC AACACTAGAACAGTATGTTTTCTGCACTGTAAATG
CATTGCCAGAAACAAC TGCTGACATTGTAGTCTTTGATGAAATCTCTATG
GCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTTCGTGCAAAACA
CTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCGCACATTGC
TGACTAAAGGCACACTAGAACCCAGAATATTTTAATTCAGTGTGCAGACTT
ATGAAAACAATAGGTCCAGACATGTTCCCTTGGAAC TTGTCGCCGTTGTCC
TGCTGAAATTGTTGACACTGTGAGTGCTTTAGTTTATGACAATAAGCTAA
AAGCACACAAGGATAAGTCAGCTCAATGCTTCAAAATGTTCTACAAAGGT
GTTATTACACATGATGTTTCATCTGCAATCAACAGACCTCAAATAGGCGT
TGTAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTGTTTTTA
TCTCACCTTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTG
CCTACGCAGACTGTTGATTTCATCACAGGGTTCTGAATATGACTATGTCAT
ATTCACACAAAAC TACTGAAACAGCACACTCTTGTAATGTCAACCGCTTCA
ATGTGGCTATCACAAGGGCAAAAATTGGCATTTTGTGCATAATGTCTGAT
AGAGATCTTTTATGACAAACTGCAATTTACAAGTCTAGAAATACCACGTGCG
CAATGTGGCTACATTACAAGCAGAAAATGTAAC TGGACTTTTTTAAGGACT
GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTC
AGCGTTGATATAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAGG
CATACCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCA
AAATGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAA
GAAGCTATTTCGTACGTTTCGTGCGTGGAATTGGCTTTGATGTAGAGGGCTG
TCATGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGAT
TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACT
GAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGA
CCAGTTTAAACATCTTATACCAC TCATGTATAAAGGCTTGCCCTGGAATG
TAGTGCGTATTAAGATAGTACAAATGCTCAGTGATACACTGAAAGGATTG
TCAGACAGAGTCGTGTTTCGTCCCTTTGGGCGCATGGCTTTGAGCTTACATC
AATGAAGTACTTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTG
ACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGG
AATCATCTCTGTGGGTTTTGACTATGTTCTATAACCCATTTATGATTGATGT
TCAGCAGTGGGGCTTTACGGGTAACCTTCAGAGTAACCATGACCAACATT
GCCAGGTACATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACT
AGATGTTTAGCAGTCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGT
TGAATACCC TATTATAGGAGATGAACTGAGGGTTAATCTGCTTGCAGAA
AAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCA
GTTCTTCATGACATTGGAAATCCAAAGGCTATCAAGTGTGTGCCTCAGGC
TGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGACAAAGCTT
ACAAAATAGAGGAAC TCTTCTATTCTTATGCTACACATCAGATAAAATTC
ACTGATGGTGTGTTGTTTGTGTTTGGAA TTGTAACGTTGATCGTTACCCAGC
CAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAAC TTGAACT
TACCAGGCTGTGATGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCAC
ACTCCAGCTTTTCGATAAAAAGTGCATTTACTAATTTAAAGCAATTGCCTTT
CTTTTACTATTCTGATAGTCCCTTGTGAGTCTCATGGCAAACAAGTAGTGT
CGGATATTGATTATGTTCCACTCAAATCTGCTACGTGTATTACACGATGC
AATTTAGGTGGTGTCTGTTTGCAGACACCATGCAAATGAGTACCGACAGTA
CTTGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTT
ACAAACAATTTGATACTTATAACCTGTGGAATACATTTACCAGGTTACAG
AGTTTAGAAAATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGG
ACACGCCGCGCAAGCACCTGTTTCCATCATTAATAATGCTGTTTACACAA
AGGTAGATGGTATTGATGTGGAGATCTTTGAAAATAAGACAACACTTCCT
GTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTAAACCAGTGCC
AGAGATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTG
TAATCTGGGACTACAAAAGAGAAGCCCCAGCACATGTATCTACAATAGGT
GTCTGCACAATGACTGACATTGCCAAGAAACCTACTGAGAGTGCTTGTTT
TTCACTTACTGTCTTGTTTGTGATGGTAGAGTGGAAGGACAGGTAGACCTTT

FIGURE 11G

TTAGAAACGCCCGTAATGGTGTTTTAATAACAGAAGGTTTCAGTCAAAGGT
CTAACACCTTCAAAGGGACCAGCACAAAGCTAGCGTCAATGGAGTCACATT
AATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACG
GCATTATTCAACAGTTGCCTGAAACCTACTTTACTCAGAGCAGAGACTTA
GAGGATTTTAAAGCCCAGATCACAATGGAACTGACTTTCTCGAGCTCGC
TATGGATGAATTCATACAGCGATATAAGCTCGAGGGCTATGCCCTCGAAC
ACATCGTTTATGGAGATTTTCAGTCATGGACAACCTGGCGGTCTTCATTTA
ATGATAGGCTTAGCCAAGCGCTCACAAAGATTCACCAC'TAAATTAGAGGA
TTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAACAGATGCGC
AAACAGGTTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGAT
GACTTTGTGCGAGATAATAAAGTCACAAGATTTGTTCAGTGATTTCAAAGT
GGTCAAGGTTACAATTGACTATGCTGAAATTTTCATTCATGCTTTGGTGTA
AGGATGGACATGTTGAAACCTTCTACCCAAAAC'TACAAGCAAGTCAAGCG
TGGAACCCAGGTGTTGCGATGCCTAACTTGTACAAGATGCAAAGAATGCT
TCTTGAAAAGTGTGACCTTCAGAATTATGGTGAAAATGCTGTTTATACCAA
AAGGAATAATGATGAATGTGCGCAAAGTATACTCAACTGTGTCAATACTTA
AATACACTTACTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTGG
TGCTGGCTCTGATAAAGGAGTTGCACCAGGTACAGCTGTGCTCAGACAAT
GGTTGCCAACTGGCACACTACTTGTGCTGATTCAGATCTTAATGACTTCGTC
TCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGC
TAATAAATGGGACCTTATTATTAGCGATATGTATGACCCTAGGACCAAAC
ATGTGACAAAAGAGAATGACTCTAAAGAAGGGTTTTTCACTTATCTGTGT
GGATTTATAAAGCAAAAAC'TAGCCCTGGGTGGTTCTATAGCTGTAAAGAT
AACAGAGCATCTTTGGAATGCTGACCTTTACAAGCTTATGGGCCATTCT
CATGGTGGACAGCTTTTGTGTACAAATGTAAATGCATCATCATCGGAAGCA
TTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAATTGATGG
CTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCC
AGTTGTCTTCTTATTCACTCTTTGACATGAGCAAATTTCTCTTAAATTA
AGAGGAAC'TGCTGTAATGTCTCTTAAGGAGAATCAAATCAATGATATGAT
TTATTCCTCTTCTGGAAGAGGTAGGCTTATCATTAGAGAAAACAACAGAG
TTGTGGTTTCAAGTGATATCTTGTTAACAACTAAACGAACATGTTTATT
TTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTGACCGGTGCAC
CACTTTTGTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTA
TGAGGGGGGTTTACTATCCTGATGAAATTTTTTAGATCAGACACTCTTTAT
TTAACTCAGGATTTATTTCTTCCATTTTATTCTAATGTTACAGGGTTTCA
TACTATTAATCATAACGTTTGGCAACCCCTGTCATACCTTTTAAAGGATGGTA
TTTATTTTGTGCTGCCACAGAGAAATCAAATGTTGTCCGTGGTTGGGTTTTT
GGTCTTACCATGAACAACAAGTCACAGTCGGTGATTATTATTAACAATTC
TACTAATGTTGTTATACGAGCATGTAAC'TTTGAATTGTGTGACAACCCCTT
TCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTC
GATAATGCATTTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCT
TGATGTTTCAGAAAAGTCAGGTAATTTTAAACACTTACGAGAGTTTGTGT
TTAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAACCTATA
GATGTAGTTTCGTGATCTACCTTCTGGTTTTTAACACTTTGAAACCTATTTT
TAAGTTGCCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAG
CCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCTGCAGCCTATTTT
GTTGGCTATTTAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGG
TACAATCACAGATGCTGTTGATGTTCTCAAATCCACTTGCTGAAC'TCA
AATGCTCTGTTAAGAGCTTTGAGATTGACAAAGGAATTTACCAGACCTCT
AATTTCAAGGGTTGTTCCCTCAGGAGATGTTGTGAGAT'TCCCTAATATTAC
AACTTGTGTCTTTTTGGAGAGGTTTTTAATGCTACTAAATTCCTTCTG
TCTATGCATGGGAGAGAAAAAAATTTCTAATTGTGTGTGCTGATTACTCT
GTGCTCTACAAC'TCAACATTTTTTCAACCTTTAAGTGCTATGGCGTTTC
TGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGCTATGCAGATTCTT
TTGTAGTCAAGGGAGATGATGTAAGACAAATAGCGCCAGGACAAACTGGT
GTTATTGCTGATTATAATTATAAATGCCAGATGATTTTCATGGGTTGTGT
CCTTGCTTGGAACTACTAGGAACATGATGCTACTTCAACTGGTAATTATA

FIGURE 11H

ATTATAAATATAGGTATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGA
GACATATCTAATGTGCCTTTCTCCCCTGATGGCAAACCTTGCACCCACC
TGCTCTTAATTTGTTATTGGCCATTAAATGATTATGGTTTTTACACCACTA
CTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACCTT
TTAAATGCACCGGCCACGGTTTGTGGACCAAAATTATCCACTGACCTTAT
TAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTG
TGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGT
GATGTTTCTGATTTCACTGATTCCGTTTCGAGATCCTAAAACATCTGAAAT
ATTAGACATTTTACCTTTCGCTTTTGGGGGTGTAAGTGTAATTACACCTG
GAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGC
ACTGATGTTTCTACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCG
CATATATTTCTACTGGAAACAATGTATTCCAGACTCAAGCAGGCTGTCTTA
TAGGAGCTGAGCATGTGACACTTCTTATGAGTGCGACATTCCTATTGGA
GCTGGCATTGTGTGCTAGTTACCATAACAGTTTCTTTATTACGTAGTACTAG
CCAAAAATCTATTGTGGCTTATACATATGCTTTTAGGTGCTGATAGTTCAA
TTGCTTACTCTAATAACACCATTGCTATACCTACTAACTTTTCAATTAGC
ATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTG
TAATATGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCC
AATATGGTAGCTTTTGCACACAACCTAAATCGTGCACCTCTCAGGTATTGCT
GCTGAACAGGATCGCAACACACGTGAAGTGTTTCGCTCAAGTCAAACAAAT
GTACAAAACCCCAACTTTGAAATATTTTGGTGGTTTTAATTTTTCACAAA
TATTACCTGACCCTCTAAAGCCAACCTAAGAGGTCTTTTATTGAGGACTTG
CTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAGCAATATGG
CGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGT
TCAATGGACTTACAGTGTGTGCCACCTCTGCTCACTGATGATATGATTGCT
GCCTACACTGCTGCTCTAGTTAGTGGTACTGCCACTGCTGGATGGACATT
TGGTGCTGGCGCTGCTCTTCAAATACCTTTTGTCTATGCAAATGGCATATA
GGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCACAAAA
CAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAGAATCACT
TACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGA
ATGCTCAAGCATTAACACACTTGTAAACAACCTAGCTCTAATTTTGGT
GCAATTTCAAGTGTTGCTAAATGATATCCTTTTCGCGACTTGATAAAGTCTGA
GGCGGAGGTACAAATGACAGGTTAATTACAGGCAGACTTCAAAGCCTTC
AAACCTATGTTAACACAACTAATCAGGGCTGCTGAAATCAGGGCTTCT
GCTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAATCAAA
AAGAGTTGACTTTTGTGGAAAGGGCTACCACCTTATGTCCTTCCCACAAG
CAGCCCCGCATGGTGTGTCTTCTTACATGTCACGTATGTGCCATCCCAG
GAGAGGAACCTTACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATA
CTTCCCTCGTGAAGGTGTTTTTGTGTTTAAATGGCACTTCTTGGTTTATTA
CACAGAGGAACCTTCTTTTCTCCACAAATAATTACTACAGACAATACATTT
GTCTCAGGAAATTTGTGATGTGCTTATTGGCATCATTAACAACACAGTTTA
TGATCCTCTGCAACCTGAGCTTGACTCATTTCAAAGAAGAGCTGGACAAGT
ACTTCAAAAATCATACATCACCAGATGTTGATCTTGGCGACATTTCAAGC
ATTAACGCTTCTGTGCTCAACATTCAAAAAGAAATTGACCGCCTCAATGA
GGTCGCTAAAAATTTAAATGAATCACTCATTTGACCTTCAAGAATTGGGAA
AATATGAGCAATATATTAAATGGCCTTGGTATGTTTGGCTCGGCTTCATT
GCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTTTGTGTCATGAC
TAGTTGTTGTCAGTTGCCTCAAGGGTGCATGCTCTTGTTGGTTCTTGCTGCA
AGTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACAT
TACACATAAACGAACTTATGGATTTGTTTATGAGATTTTTTACTCTTAGA
TCAATTACTGCACAGCCAGTAAAAATTGACAATGCTTCTCCTGCAAGTAC
TGTTTCATGCTACAGCAACGATACCGCTACAAGCCTCACTCCCTTTTCGGAT
GGCTTGTTATTGGCGTTGCATTTCTTGCTGTTTTTTCAGAGCGCTACCAAA
ATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCA
GTTTCAATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTACATCTTT
TGCTTGTCGCTGCAGGTATGGAGGCGCAATTTTGTACCTCTATGCCTTG
ATATATTTTCTACAATGCATCAACGCATGTAGAATTATTATGAGATGTTG

FIGURE 11I

GCTTTGTTGGAAGTGCAAATCCAAGAACCCATTACTTTATGATGCCAACT
ACTTTGTTTGCTGGCACACACATAACTATGACTACTGTATACCATATAAC
AGTGTACACAGATACAAATTGTCGTTACTGAAGGTGACGGCATTTC AACACC
AAA ACTCAAAGAAGACTACCAAATTGGTGGTTATTCTGAGGATAGGCACT
CAGGTGTTAAAGACTATGTCGTTGTACATGGCTATTTACCCGAAGTTTAC
TACCAGCTTGAGTCTACACAAATTACTACAGACACTGGTATTGAAAATGC
TACATTCTTCATCTTTAACAAGCTTGTTAAAGACCCACCGAATGTGCAAA
TACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGCAATGGATCCA
ATTTATGATGAGCCGACGACGACTACTAGCGTGCCTTTGTAAGCACAAGA
AAGTGAGTACGAACCTTATGTACTCATTCTGTTTCGGAAGAAACAGGTACGT
TAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTTCGTGGTATTCTTGCTA
GTCACACTAGCCATCCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAA
TATTGTTAACGTGAGTTTAGTAAAACCAACGGTTTACGTCTACTCGCGTG
TTAAAAATCTGAACCTCTCTGAAGGAGTTCCTGATCTTCTGGTCTAAACG
AACTAACTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATG
GCAGACAACGGTACTATTACCGTTGAGGAGCTTAAACAACCTCCTGGAACA
ATGGAACCTAGTAATAGGTTTCTTATTCCTAGCCTGGATTATGTTACTAC
AATTTGCCTATTCTAATCGGAACAGGTTTTTGTACATAATAAAGCTTGTT
TTCCTCTGGCTCTTGTGGCCAGTAACACTTGCTTGTTTTGTGCTTGCTGC
TGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATTGCAATGGCTT
GTATTGTAGGCTTGATGTGGCTTAGCTACTTCGTTGCTTCCCTCAGGCTG
TTTGCTCGTACCCGCTCAATGTGGTCATTCAACCCAGAAAACAAACATCT
TCTCAATGTGCCTCTCCGGGGGACAATTGTGACCAGACCGCTCATGGAAA
GTGAACCTTGTCATTGGTGTGTCGATCATTCTGTTGCTCACTTGCGAATGGCC
GGACACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAGATCAC
TGTGGCTACATCACGAACGCTTTCTTATTACAAATTAGGAGCGTCGCAGC
GTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTATTGGA
AACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTT
GCTAGTACAGTAAGTGACAACAGATGTTTCATCTTGTTGACTTCCAGGTT
ACAATAGCAGAGATATTGATTATCATTATGAGGACTTTCAGGATTGCTAT
TTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATTTAAGC
CTCTAACTAAGAAGAAATTATTCGGAGTTAGATGATGAAGAACCTATGGAG
TTAGATTATCCATAAAACGAACATGAAAATTATTCTCTTCTGACATTGA
TTGTATTTTACTACTTGCAGCTATATCACTATCAGGAGTGTGTTAGAGGT
ACGACTGTACTACTATAAAGAACCTTGCCCATCAGGAACATACGAGGGCAA
TTCACCATTTACCCCTCTTGCTGACAATAAATTTGCACTAACTTGCACTA
GCACACACTTTGCTTTTGTGCTGTGCTGACGGTACTCGACATACCTATCAG
CTGCGTGCAAGATCAGTTTACCAAAACCTTTTCATCAGACAAGAGGAGGT
TCAACAAGAGCTCTACTCGCCACTTTTTCTCATTGTTGCTGCTCTAGTAT
TTTTAATACTTTGCTTCACCATTAAAGAGAAAGACAGAAATGAATGAGCTCA
CTTTAATTGACTTCTATTGTGCTTTTTAGCCTTTCTGCTATTCCCTTGTT
TTAATAATGCTTATTATATTTTGGTTTTTCACTCGAAATCCAGGATCTAGA
AGAACCTTGTACCAAAGTCTAAACGAACATGAAACTTCTCATTGTTTTGA
CTTGATTTTCTCTATGCAGTTGCATATGCACTGTAGTACAGCGCTGTGCA
TCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGG
GTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAAGGTTTTACCT
TTTCATAGATGGCACACTATGGTTCAAACATGCACACCTAATGTTACTAT
CAACTGTCAAGATCCAGCTGGTGGTGCCTTATAGCTAGGTGTTGGTACC
TTCATGAAGGTCACCAAACCTGCTGCATTTAGAGACGTACTTGTGTTTTA
AATAAACGAACAAAATTAAAATGTCTGATAATGGACCCCAATCAAACCAAC
GTAGTGCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAAT
AACCAGAATTGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCA
AGGTTTACCCTAATAACTGCGTCTTGTTTACACAGCTCTCACTCAGCATG
GCAAGGAGGAACCTTAGATTCCCTCGAGGCCAGGGCGTTCCAATCAACACC
AATAGTGGTCCAGATGACCAAATTGGCTACTACCGAAGAGCTACCCGACG
AGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACT
TCTATTACCTAGGAACCTGGCCAGAAGCTTCACTTCCCTACGGCGCTAAC

FIGURE 11J

AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAA
AGACCACATTGGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTAC
AACTTCCTCAAGGAACAACATTGCCAAAAGGCTTCTACGCAGAGGGAAGC
AGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTAA
TTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTCGAA
TGGCTAGCGGAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGACAGA
TTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAACAAGG
CCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCC
AAAAACGTACTGCCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGA
CGTGGTCCAGAACAAACCCAAGGAAATTTGCGGGACCAAGACCTAATCAG
ACAAGGAAGTGAATACAAACATTGGCCGCAAATTGCACAATTTGCTCCAA
GTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCT
TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGA
TCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCAT
ACAAAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAGACT
GATGAAGCTCAGCCTTTGCCGCGAGAGACAAAAGAAGCAGCCCACTGTGAC
TCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAACCTCAAAATT
CCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATG
ACCACACAAGGCAGATGGGCTATGTAAACGTTTTTCGCAATTCGGTTTACG
ATACATAGTCTACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACA
AGTAGGTTTtagTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGT
AACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGC
GGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAGCTGCCTATAT
GGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTG
ATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAAAAAAAAAAAAAAAAA A

GenBank Accession No. AY274119.3, SEQ ID NO: 15

FIGURE 11K

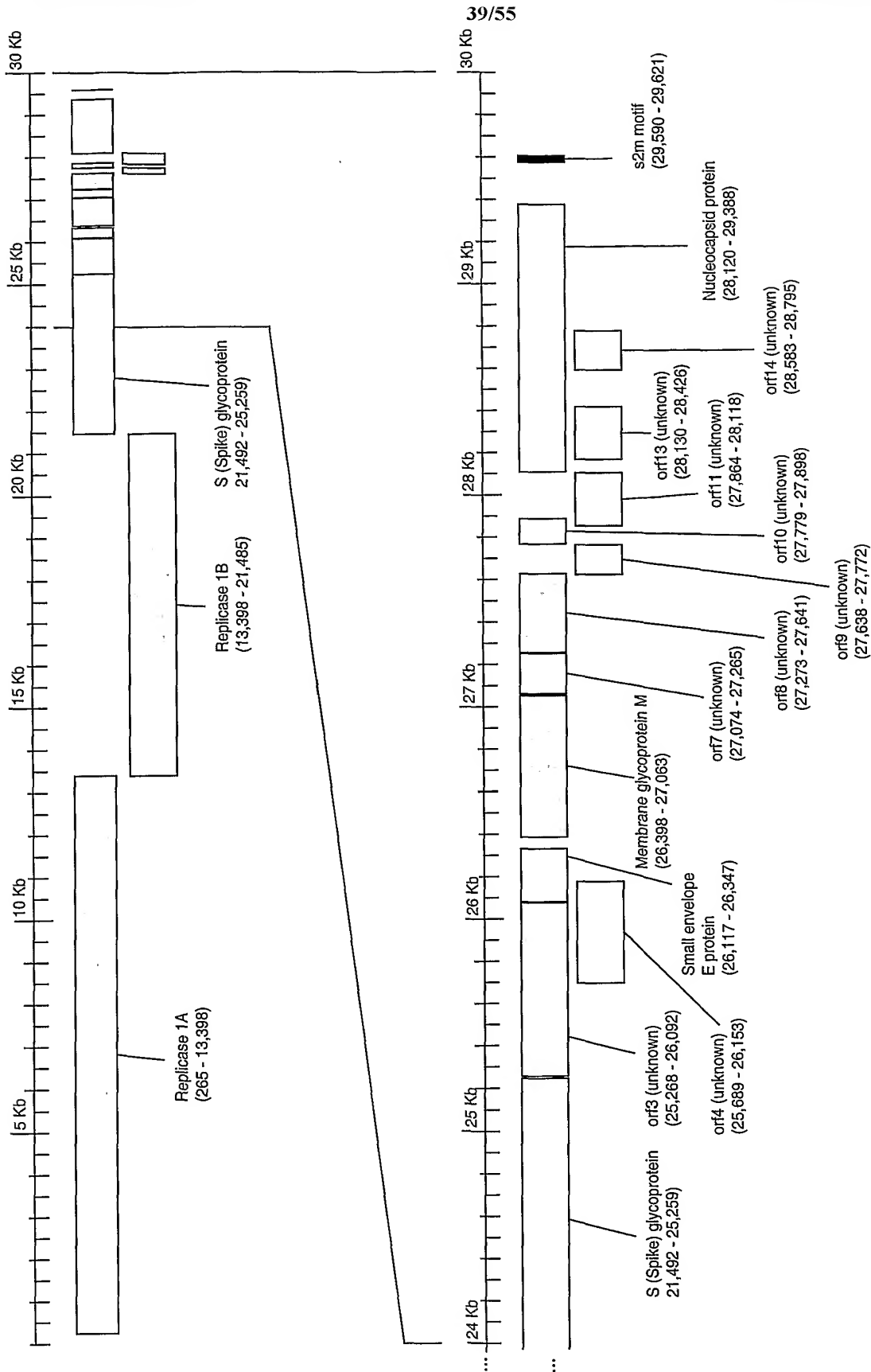


Figure 12

Replicase 1A

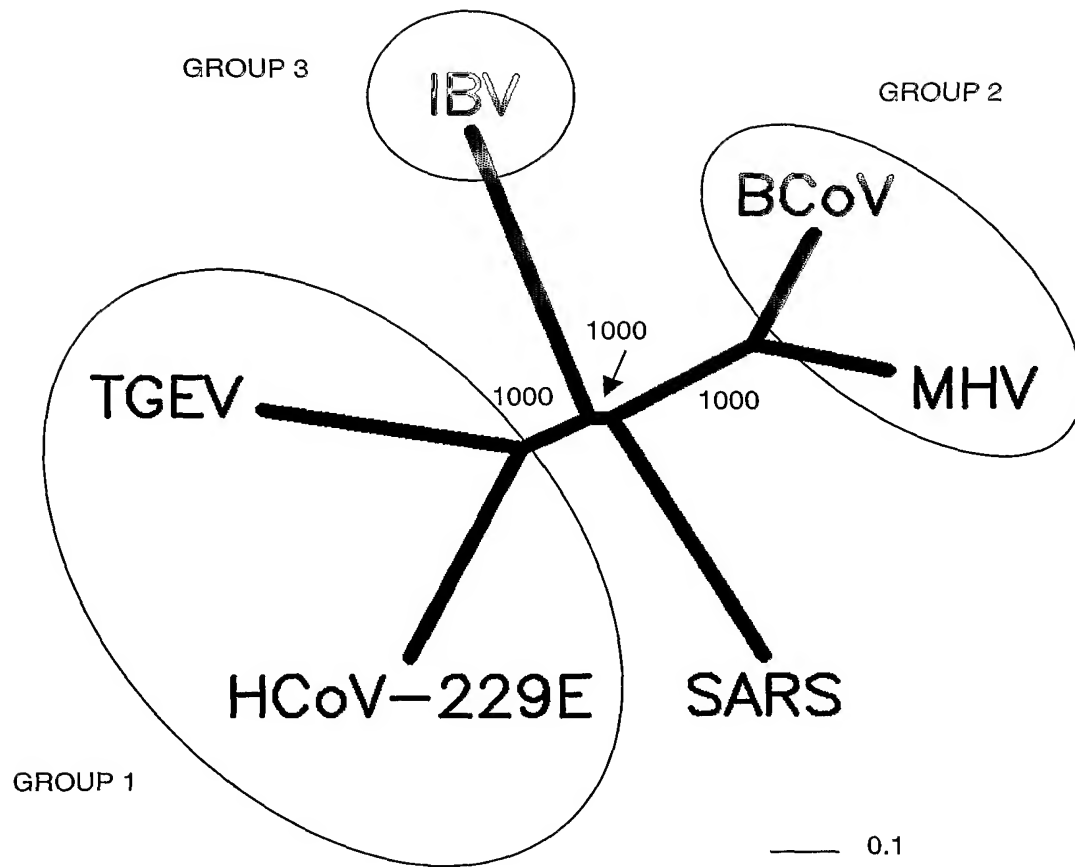


Figure 13A

Membrane Glycoprotein

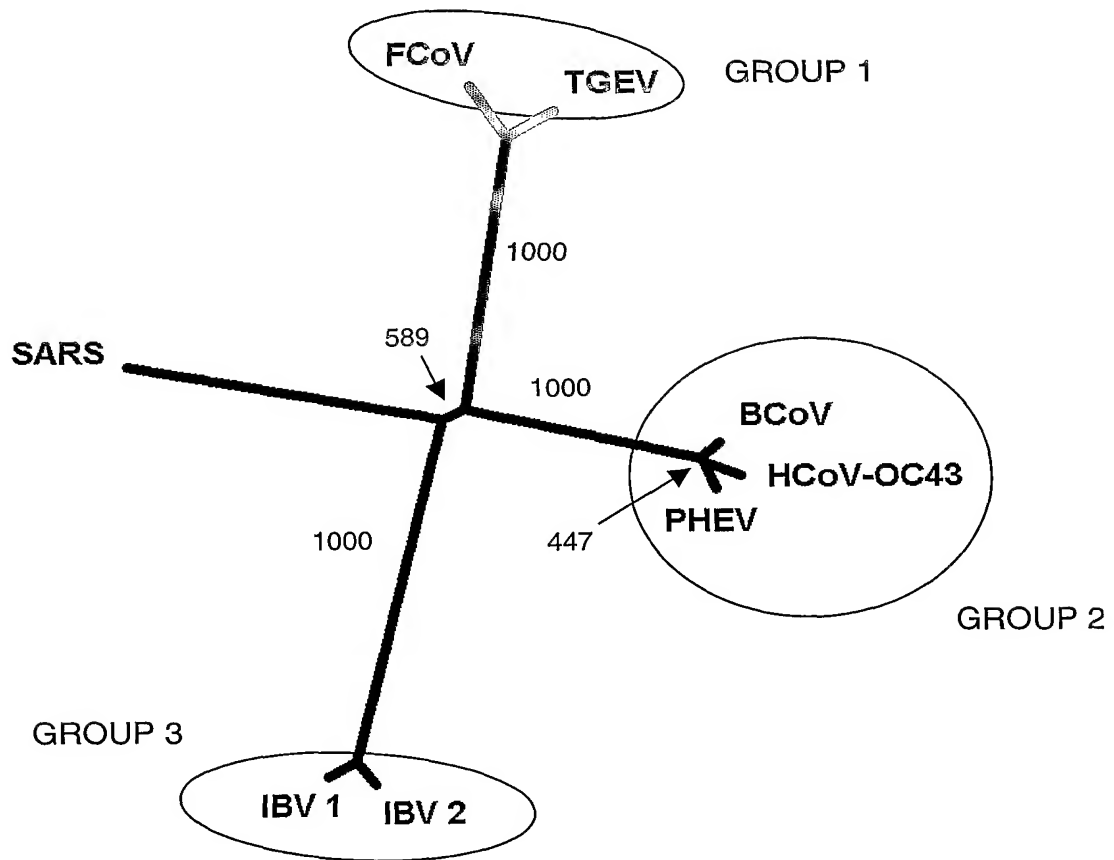


Figure 13B

Nucleocapsid

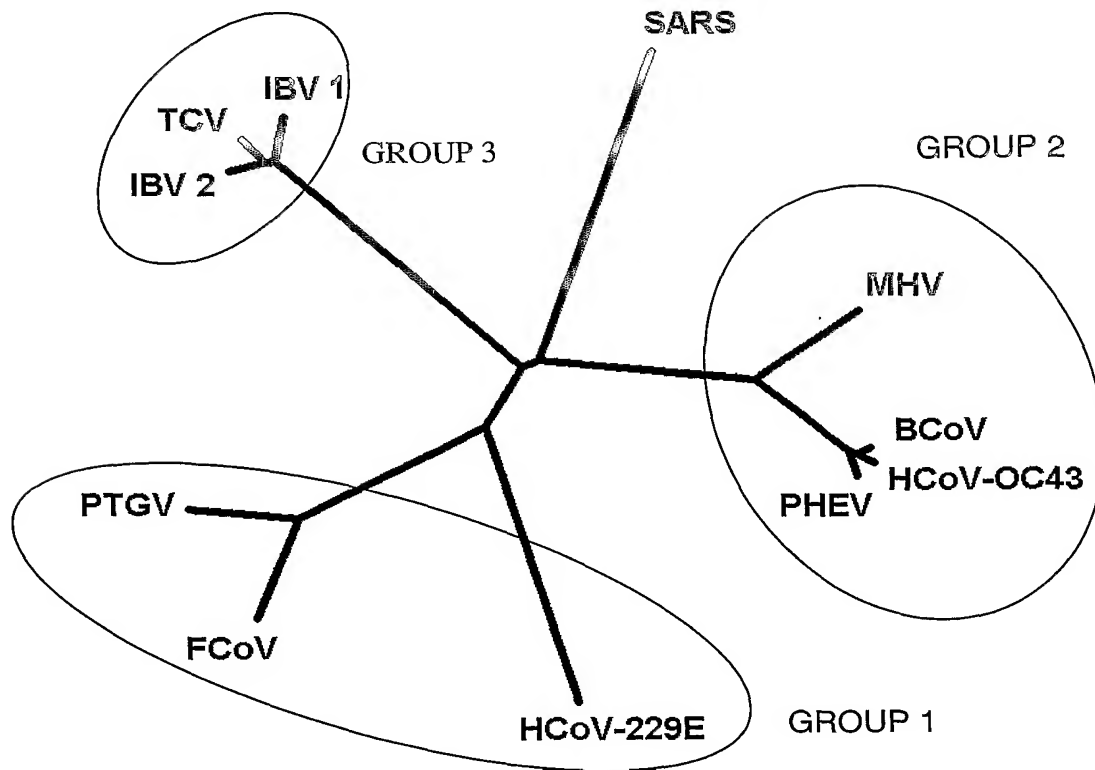


Figure 13C

S (Spike) Glycoprotein

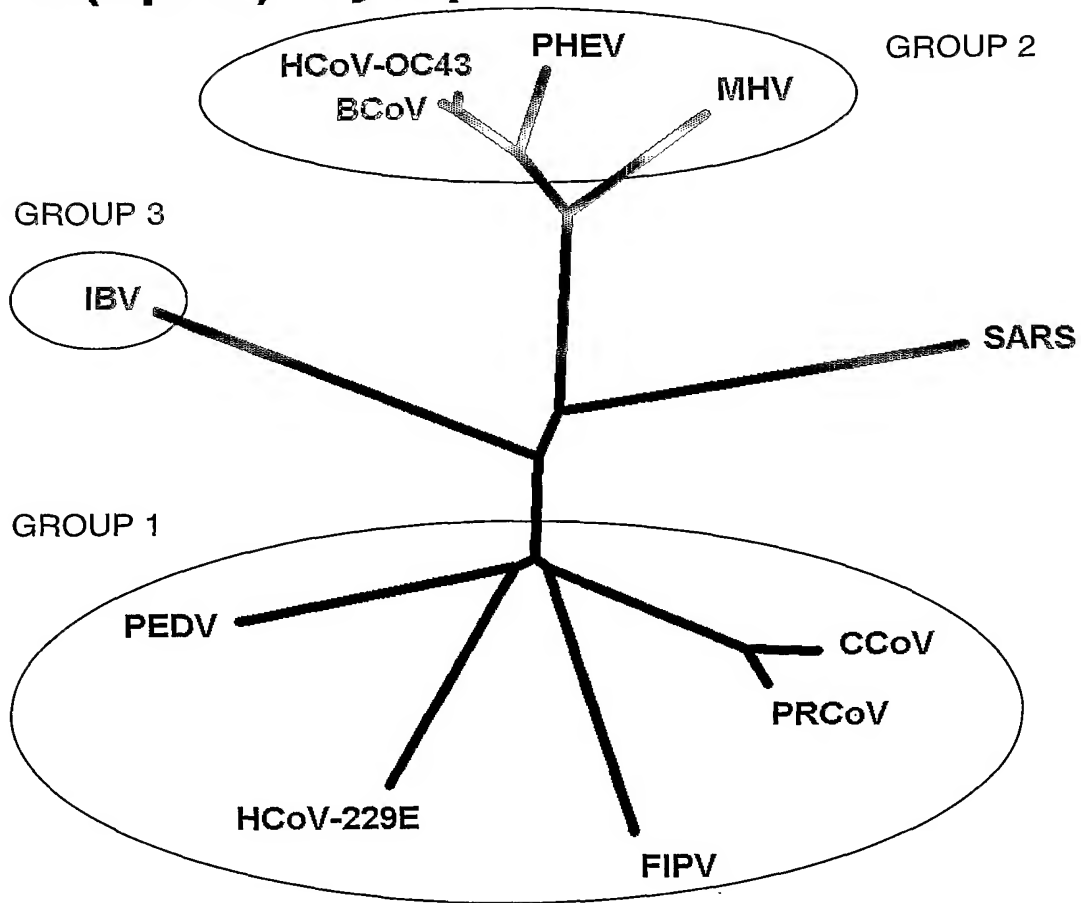


Figure 13D

```

229E -----
PEDV -----MRSLIYFWLLLPVLPPTLSLPQDVTRCQSTT-----NFRFFFSKFNVQAPA
CCov MIVLILCLLLFSYNSVICTSNNDVCVQGNVTQLPGNE-----NIIKDFLFHTFKEEP
PRC -----
FICV -----MIFIILTLLSVAKSEDAPHGVTL PQFNTSHNNERFELNFYNFLTQWDIPPNT
BoCov -----MFLILLISLPM
OC43 -----MFLILLISLPM
PHEV -----MFFILLISLPSA
MHV -----MLFVFILLLPSC
TOR2_S -----
AIBV -----

229E -----
PEDV VVVLGGYLP-----SMNSSSWYCGTGIETASGVHGIFLSYIDSGQGFE
CCov SVVVGYYPTE-----VWYNCSRSATTTAYKDFSNIHAFYFDMEMENSTG
PRC -----
FICV ETILGGYLPYCGAGVNCGWYNFSQSVGQNGKYAYINTQNLNIPNVHGVYFDVREHNDGE
BoCov FAVIGDLKCT-----TVSINDVDTGAPSIISTDIVDVTNGLG
OC43 LAVIGDLKCT-----TVAINDVDTGVPSTSTDIVDVTNGLG
PHEV FAVIGDLKCT-----TSLINDVDTGVPSSISEVVVDVTNGLG
MHV LGYIGDFRCIQ-----TVNYNGNNASAPSISTEAVDVSCKGRG
TOR2_S -----MFIFLLFLTLTSGSLLDRCTTFDDVQAPNYTQ
AIBV -----

229E -----
PEDV IG-----ISQEPFDPSPGYQLYLHKATNGNTNATARLR--ICQFPDNKTLGPTVNDVTTG-
CCov NARGKPLLHVHVGDPVSIIYISAYRDDVQPRPLLKHGLLCITKNKIIDYNTFTSAQWS-
PRC -----
FICV WDDRDKVGLLIAIHGNSKYSLLMVLQDAVEANQPHVAVKICHWKPGNISSYHAFSVNLGD
BoCov TY-----YVLDRVYLNNTLLLLNGYYPTSGSTYRNMALKGTLTLLSRLWFKPFLSDFING-
OC43 TY-----YVLDRVYLNNTLLLLNGYYPTSGSTYRNMALKGTLTLLSRLWFKPFLSDFING-
PHEV TF-----YVLDRVYLNNTLLLLNGYYPTSGATFRNMALKGTRLLSTLWFKPFLSPFNDG-
MHV TY-----YVLDRVYLNNTLLLLNGYYPTSGATFRNMALKGTRLLSTLWFKPFLSPFNDG-
TOR2_S HT-----SSMRGVYYPDEIFRSDTLTLYLTQDLFLPFYSNVTGFHTINHTFGNPVPIPKDG-
AIBV -----

229E -----
PEDV -RNCLFNKAIP--AYMRDGKDIVVGITWDNDRVT-VFADKIYHFYLNKNDWSR-----
CCov -AICLGDDRKIPFSVIPTDNGTKIFGLEWDDYVTAYISDRSHHLNINNWFNNVTILYS
PRC -----
FICV GGQCWFVNQRFS---LDTVLTNDYGFQWTDYVDIYLGGTITKVWVDNDWSIVEAS---
BoCov ----IFAKVKN----TKVIKKGVMYSEFPATIGSTFVNTSYSVVVPHTTN-----
OC43 ----IFAKVKN----TKVIKHGVMYSEFPATIGSTFVNTSYSVVVPHTTN-----
PHEV ----IFAKVKN----SRFSKDGVIYSEFPATIGSTFVNTSYSVVVEPHTSL-----
MHV ----IFAKVQN----LKTNTPTGATSYFPPTIVIGSLFGNTSYTVVLEPYNN-----
TOR2_S ---IYFAATEK-----SNVVRGWVFGSTMNKSQSVIINNSTNVVIRACNFELCDN---
AIBV -----MLGKSLFLVTILCALCSANLFDPPANYVYYYQSAFRP-----

229E -----MFVLLVAYALLHIAGCQTTNGLN--TSYSVCNG---CVGYSENVFAVES
PEDV --VATRCYNRRSCAMQYVYPTTYMLNVT SAGEDG-IYEPCTAN--CTGYAANVFATDS
CCov RSSSATWQKSAAYVYQGVSNFTYYKLNNTNGLKS----YELCEDYEYCTGYATNVFAPTV
PRC -----MKKLFVVLVVMPLIYGDKEFTSVVSN-----CTD--QCASYVANVFETQP
FICV -ISYHWNRIYGYVMQFVNRTTYAYNNTGGANYTQLQLSECHTD-YCAGYAKNVFVP-I
BoCov -LDNKLQGLLEISVCQYTMCEYPHTICHPNL-GNKRVELWHWDTG VVSCLYKRNFYDYN
OC43 -LDNKLQGLLEISVCQYTMCEYPHTICHPNL-GNRRVELWHWDTG VVSCLYKRNFYDYN
PHEV -INGNLQGLLQISVCQYTMCEYPHTICHPNL-GNQRIELWHYDTDVVSCLYRRNFYDYN
MHV -----IIMASVCTYTICQLPYTPCKPNTNGNRVIGFWHTDVKPPICLLKRNFYFNVN
TOR2_S ---PFFAYSKPMGTQTHMTMIFDNAPNCTFEYISDAFSLDVSEKSGNFKHLREFVFNKDG
AIBV -----SNGWHLQGGAYAVVNSNYANNAGSASECT--VGVIKDVYNQSAASIAMTAPLQG

```

FIGURE 14A

229E GGYIPSDFAFNN--WFLLTNTSSVVDGVVRSFQPLLLNCLWSVSGLRFTTGFFVYFNGTGR
 PEDV NGHIPEGFSFNN--WFLLSNDSTLLHGKVVSNQPLLVNCLLAIPKIYGLGQFFSFNHTMD
 CCov GGYIPHGFSFNN--WFMRTNSSTFVSGRFVTNQPLLVNCLWPVPSPFGVAAQQCFEGAGQF
 PRC GGFIPSDFSFNN--WFLLTNSSTLVSGKLVTKQPLLVNCLWPVPSPFEEAATFCFEGADP
 FICV DGKIPEDFSFNN--WFLLSDKSTLVQGRVLSSQPVFVQCLRPVPSWSNNTAVVHFKN-D
 BoCov ADYLYFHFYQEGGTFYAYFTDTGTVTKFLFNVYLGTVLSHYVYVPLTCS----SAMTLEY
 OC43 ADYLYFHFYQEGGTFYAYFTDTGTVTKFLFNVYLGTVLSHYVYVPLTCS----SAMTLEY
 PHEV ADYLYFHFYQEGGTFYAYFTDTGTVTKFLFNVYLGTVLSHYVYVPLTCS----SALSLEY
 MHV APWLYFHFYQGGTFYAYYADKPSATTFLEFSVYIGDILTQYFVLFFICTPTAGSTLAPLY
 TOR2_S FLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAY
 AIBV MAWSKSQFSAHCDSEITVVFTHCYSSGSGSCPITGMIARGHIRISAMKNGSLFYNLTV

:

229E GDCKGFSDDVLSDVIRYNLN-FEENLRRT-----ILFKTSYGV-VVFYCTNNT-----
 PEDV GVCNGAAVDRAPALRFNINDTVSILAECS-----IVLHTALGTNLSTFVCSNSSD-----
 CCov SQCNGVSLNNTVDVIRFNLN-FTALVQSGMGATV-FSLNTTGGVILEISCYNDTVS---E
 PRC DQCNGAVLNNTVDVIRFNLN-FTTNVQSGKGATV-FSLNTTGGVILEISCYNDTVS---D
 FICV AFCP-----NVTADVLRFNLFSDTDVYTDSTNDEQLFFTFEDNTASIAICYSSANVDFQ
 BoCov WVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMS---EIKCKTSLIAPSTGVYELNG-----
 OC43 WVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMS---EIKCKTSLIAPSTGVYELNG-----
 PHEV WVTPLTTRQFLAFDQDGVLYHAVDCASDFMS---EIMCKTSSITPPTGVYELNG-----
 MHV WVTPLTKRQYLFNFNEKGVITSAVDCASSYIS---EIKCKTQSLPSTGVYDLG-----
 TOR2_S FVGYLKPTTFMLKYDENGITIDAVDCSQNPLA---ELKCSVKSFEDKGIYQTSN-----
 AIBV SVSKYPNFKSFQCVNNFTSVYLNGLVFTSNKTTDVTSGVYFKAGGPVNYSIMK-----

229E -LVSGDAHIFPGTVLGNFYCFVNTTIGTETTSAFVGALEPKTVREFVISRTGHFYINGYRY
 PEDV -PHLAIFAIPLGATEVPYCYFLKVDTYNSTVYKFLAVLPSTVREIVITKYGDVYVNGFGY
 CCov SSFYSGEISFGVTDGPRYCF--LYNGTALKYLGTLPPSVKEIAISKWGHFYINGYNYF
 PRC SSFSSYGEIPFGVTNGPRYCV--LYNGTALKYLGTLPPSVKEIAISKWGHFYINGYNYF
 FICV PANNSVSHIPFGKT--AHFCFAN-FSHSIVSRQFLGILPPTVREFAFGRDGSIFVNGYKY
 BoCov -YTVQPIADVYRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSSNCFNMSSLSMFIQADS
 OC43 -YTVQPIADVYRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSSNCFNMSSLSMFIQADS
 PHEV -YTVQPVATVYRRIPLPNCIDIEAWLNSKTIVSSPLNWERKIFSSNCFNMGRMMSFIQADS
 MHV -YTVQPVGVYRRIPNLPDCNIEEWLTAKSVPSPPLNWERRTFQNCNENLSSLLRYVQAES
 TOR2_S -FRVVPSPGDVVRFPNITNLCPFGEVFNATKFPVYAWERKKISNCVADYSVLYNSTFFST
 AIBV -EFKVLAYFVNGTAQDVLCDNSPKGLLACQYNTGNFSDGFYPTNSTLVREKFIVYRES

*

229E FTILGNVEAVNFNVTTAETTD---FFTVALASYADVLVNSQTSIANIYYCNSVINRLRC
 PEDV LHLGLLDVATYFTGHGTDDBDVSGFWTIASTNFVDALIEVQGTSTQRILYCDPVSQKLC
 CCov FSTFPIDCISFNLTTGDSGA---FWTIAYSYTDALVQVENTAIKKVTCNSHINNICK
 PRC FSTFPIDCISFNLTTGDSV---FWTIAYSYTEALVQVENTAITNVTYCNYSVNNICK
 FICV FSLPAIRSVNFSSISVEEYG---FWTIAYTNYTDMVDVNGTATRLFYCDSPLNRIKC
 BoCov FTCNNIDAANKIYGMCFSSIT---IDKFAIPNGRKVDLQGLNGLYLSFNRYIDTTATSC
 OC43 FTCNNIDAANKIYGMCFSSIT---IDKFAIPNGRKVDLQGLNGLYLSFNRYIDTTATSC
 PHEV FGCNNIDASRLYGMCFGSIT---IDKFAIPNSRKVDLQVGKSGYLSFNRYKIDTAVSSC
 MHV LSCNNIDASKVYGMCFGSVS---VDKFAIPRSRQIDLQIGNSGFLQTANYKIDTATSC
 TOR2_S FKCYGVSAKLNLCFSNVY---ADSFVVKGDVVRQIAPGQTGVIADYNYKLPDDFMGC
 AIBV SVNTTLALTNTFTTNVSNAQ---PNSGGVHTFHLVYQTQTAQSGYYNFNLSFLSQFVYKA

:

229E DQLSFYVPDGFYSTSP--IQSVELPVSIVSLP-----VYHKHMFIVLYVDFKPKQ---
 PEDV SQVAFDLDDGFYPISSRNLLSHEQPISFVTLP-----SFNDHSFVNITVSA-----
 CCov SQTANLQNGFYPVAS--SEVGLVNKSVVLLP-----SFYHSTSVNITIDLGMKR--
 PRC SQTANLNNGFYPVSS--SEVGSVNKSVVLLP-----SFLTHTIVNITIGLGMKR--
 FICV QQLKHELDPGFYSASM--LVKKDLPKTFVTMP-----QFYHWMNVTLHVVLNDTEKK
 BoCov -QLYYNLPAAVSVSRFNPSTWNRFGFTEQVFVKPQPVGVFTHHDVVYAQHCFAKPNF
 OC43 -QLYYNLPAAVSVSRFNPSTWNRFGFTEQSVFVKPQPVGVFTHHDVVYAQHCFAKPNF
 PHEV -QLYYSLPAANVSVTHYNPSSWNRRYGFNNQS-----FGSRGLHDAVYSQCCFNTPTNY
 MHV -QLYYSLPKMNVTTINYNPSSWNRRYGFKNV-----
 TOR2_S -VLAWNTRNIDATSTG---Nynykyrylrhg-----
 AIBV SDYMYGSYHPICAFRP---ETINSGLWFNSLS-----

FIGURE 14B

```

229E      ---SGGKCFNCYPAGVNITLANFNETKG---PLCVDTSHFT-----TKYVAVYAN
PEDV      ---FGGLSSANLVAS--DPTINGFSS-----FCVDTRQFTI-----TLFYNVTNS
CCov      ---SGYGQPIASTLS--NITLPMQDNNTD---VYCIRSNRFSVYFHSCTCKSSLWDDVFNS
PRC       ---SGYGQPIASTLS--NITLPMQDNNTD---VYCVRSDDQFSVYVHSTCKSALWDNVFKR
FICV      YDIILAKAPELAALADVHFEBIAQANGSVTNVTSCLCVQARQLA-----LFYKYTSL
BoCov     --CPCKLDGSLCVGNGPGIDAGYKNSGIG---TCPAGTNYLT---CHNAA---QCDC
OC43      --CPCKLDGSLCVGNGPGIDAGYKNSGIG---TCPAGTNYLT---CHNAV---QCNC
PHEV      --CPCRT--SQCIQ---G-----AGTG---TCPVGTTRVK---CFAAVTKATKCTC
MHV       -----
TOR2_S    -----
AIBV      -----

229E      ----VGRWSASINTGNCPPSFGKVNMFVKFSGVCFSLKDIPGG-CAMPIVANWAYSKEYYT
PEDV      ----YGVVSKSQDS-NCPFTLQSVNDYLSFSKFCVSTSLLAGA-CTIDLFGYPAGSGVK
CCov      DCTDVLVYATAVIKTGTCTPFSFDKLNMYLTFNKFCLSLNPVGAN-CKFDVAARTRTNEQVV
PRC       NCTDVLDATAVIKTGTCTPFSFDKLNMYLTFNKFCLSLNPVGAN-CKFDVAARTRTNEQVV
FICV      QGLYTYSNLVELQNYDCPFSPPQFNMYLQFETLCLCFDVNPAVAG-CKWSLVHVDQWRTQFA
BoCov     LCTPDPITSKSTGPYKCPQTKYLVGIGEHCSEGLAIKSDYCGGNPCTCQPAFLGWSVDSC
OC43      LCTPDPITSKSTGPYKCPQTKYLVGIGEHCSEGLAIKSDYCGGNPCTCQPAFLGWSVDSC
PHEV      WCQPDSTYKGVNAWTCQSKVSIQPGQHCPGLGLVEDDCSGNPCTCKPQAFIGWSSETC
MHV       -----
TOR2_S    -----
AIBV      -----KLR-----PFERDISN--VPFSPDGKCTPPALN-CYWPLNDYGFYTTTGI
          -----VSLTYGPLQGGYKQSVFSGKATCCYAYSNGPRACKGVYSGELSRDFECG

229E      IG----TLYVSWSDGDGITGVPQ-PVEGVSSFMNVTLDKCTKYNIYDVSGVGIRVSNdT
PEDV      LT----SLYFQFTKGELITGTPK-PLEGITDVSFMTLDVCTKYTIYGFKEGEGITLTNSS
CCov      R-----SLYVIYEEGDNIYGVPS-DNSGLHDLVLHLDSCTDYNIYGITGVGIIRQTNST
PRC       R-----SLYVIYEEGDNIYGVPS-DNSGLHDLVLHLDSCTDYNIYGRGVGIIRQTNST
FICV      T-----ITVSYKHGSMITTHAKGHSWGFQDTSVLVKDECTDYNIYGFQGTGIIRNTTSR
BoCov     LQGDRCNIFANFIFHDVNSGTTT-STD LQKSNTDIILGVCVNYDLYGITGQGIFVEVNAT
OC43      LQGDRCNIFANFILHDVNSGTTT-STD LQKSNTDIILGVCVNYDLYGITGQGIFVEVNAT
PHEV      LQNGRCNIFANFILNDVNSGTTT-STD LQQNTIITTDVCVNYDLYGITGQGLIEVNAT
MHV       ---RCQIFANILLNGINSGTTT-STD LQLEPTEVATGVCVRYDLYGITGQGVFKEVKAD
TOR2_S    G----YQPYRVVLSFELLNAPA-TVCGPKLSTD LKNCQCNFNFNGLTGTGVLTPSSKR
AIBV      L-----LVYVTKSDGSRIRQTRTEPLVLTQHNNITLTKCVAYNIYGRVQGFITNVNDS
          .          .          .          .          .          .          .          .
          :          .          *          .          .          .          .          .

229E      FLN-----GITYTSTSGNLLGFKDVTGKIYISITPCNP---PDQLVVYQQAVVGAM
PEDV      ILA-----GVYYSDSGQLLAFKNVTSAGVYSVTPCSF---SEQAAYVNDIDVIGVI
CCov      LLS-----GLYYTSLSGDLLGFKNVSDGVIYSVTPCDV---SAHAAVIDGAIVGAM
PRC       LLS-----GLYYTSLSGDLLGFKNVSDGVIYSVTPCDV---SAQAAVIDGITVGA
FICV      LVA-----GLYYTSLSGDLLAFKNSTTGEIFTVVPCLD---TAQVAVINDEIVGAI
BoCov     YYNS-----WQNLLYDSNGNLYGFRDYL TNRTFMIRSCYSG--RVSAAFHANSSEPAL
OC43      YYNS-----WQNLLYDSNGNLYGFRDYL TNRTFMIRSCYSG--RVSAAFHANSSEPAL
PHEV      YYNS-----WQNLLYDSNGNLYGFRDYL TNRTFMIRSCYSG--RVSAVAFHANSSEPAL
MHV       YYNS-----WQALLYDVNGNLNGFRDL TNKTYTIRSCYSG--RVSAAYHKEAPEPAL
TOR2_S    FQP-----FQQFGRDVSDFDTSVRDPKTSEILDISPACFGGVSVITPGTNASSEVAV
AIBV      VANFSYLADGGLAILDTS GAIDVFVVGSGYGLNYYKVNPCEDVN--QQFVVSGGNIVGIL
          .          .          .          .          .          .          .          .
          :          .          *          .          .          .          .          .

229E      LSENFTSY-----GFSNVVELPKFFYASNGTYN-----
PEDV      SLSNST-----FNNTRELPGFYHSDNGSN-----
CCov      TSINSELL-----GLTHWTTTPNFYYYSTYNYTNERTRGTAID--SND
PRC       TSINSELL-----GLTHWTTTPNFYYYSTYNYTNNDKTRGTPID--SND
FICV      TAVNQTDLFEFVNNTQARRSRSTPNFVTSYTMPQFYIITKWNNDTS-S-----
BoCov     LFRNIKN-----YVFNNTLRQLQPINYFDSYLGCVVNADN-----STS
OC43      LFRNIKN-----YVFNNTLRQLQPINYFDSYLGCVVNADN-----STA
PHEV      MFRNLKCS-----HVFNNTLRQLQPINYFDSYLGCVVNAYN-----NTA
MHV       LYRNINCS-----YVFNNISREENPLNYFDSYLGCVVNADN-----RTD
TOR2_S    LYQDVNCT-----DVSTAIHADQLTPAWRIYSTGNVVFQTOAGCLIGAHEV
AIBV      TSRNETGS-----E-QVENQFYVKLTNSSHRRRS-----IG

229E      -CTDAVLTYSSFGVCADGSIIAVQ-----PRNVSYDSVSAIVTANLS-----
PEDV      -CTEPVLVYSNIGVCKSGSIGYV-----PSQYQVQKIAPTVTGNIS-----
CCov      VDCEPIITYSNIGVCKNGALVFI-----NVTHSDGDVQPISTGNVT-----
PRC       VGCEPIITYSNIGVCKNGALVFI-----NVTHSDGDVQPISTGNVT-----
FICV      -NCTSAITYSSFAICNTGEIKYVNVTHVEIVDDSIGVIKPVSTGNIS-----
BoCov     SVVQTCDLTVSGYCVDYSTKRRSR-RAITGTYRFTNFEPFTVNSVNDLSLEPVGGLYEIQ

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FIGURE 14C

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OC43      SAVQTCDLTVGSGYCVDYSTKRRSR-RAITTYGYRFTNFEPFTVNSVNDLEHVGGLEYIQ
PHEV      SAVSTCDLTVGSGYCVDYVTALRSR-RSFTTYGYRFTNFEPFAANLVNDSIEPVGGLEYIQ
MHV       EALPNCNLRMGAGLCVDYSKSRRAR-RSVSTGYRLTTFEPYMPMLVNDSVQSVGGLEYEMQ
TOR2_S    DTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNN-----TIA
AIBV      QNVTSCPVSYSGRFCIEPDGSLKMI----VPEELKQFVAPLLNITES-----VL
          *

229E      IPSNWTISVQVEYLQITSTPIVVDCASTYVCNGNVRCELLKQYTSACKTIEDALRNSARL
PEDV      IPTNFTSISRTEYLQLYNTPVSVDCATYVCNGNSRCKQLLTQYTAACKTIESALQLSARL
CCov      IPTNFTISVQVEYIQVYTTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARL
PRC       IPTNFTISVQVEYIQVYTTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARL
FICV      IPKNFTTAVQAEYIQIVKPVVVDCAHYVCNGNTHCLKLLTQYTSACQTIEANLNLGARL
BoCov     IPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNEL
OC43      IPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDCAACKSQLVEYGSFCDNINAILTEVNEL
PHEV      IPSEFTIGNLLEFIQTRSPKVTIDCATFVCGDYAACRQQLAEYGSFCENINAILTEVNEL
MHV       IPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACRQQLVEYGSFCDNVNAILNEVNNL
TOR2_S    IPTNFSISITTEVMPVSMKTSVDCNMYICGDSSTECANLLQLYGSFCTQLNRALSGIAAE
AIBV      IPNSFNLTVTDEYIQTRMDKVQINCLQYVCNLSLECRKLFQYGPVCDNLSVNVSVSQK
          * . . . . . * : : : * : : * . . . . . * : :

229E      ESADVSEMLTFDKKAFTLANVSSF-GD-----YNLSSVIPS-----LPTSGSR--
PEDV      ESVEVNSMLTISEEALQLATISSFNGDG-----YNFTNVLGASVY-----DPASGRV--
CCov      ENMEIDSMFLVSENAKLASVEAFNSTETLDPIYKEWPNIGGSWLGGLKDILPSHNSK--
PRC       ENMEVDSMLFVSENAKLASVEAFNSSETLDPIYTQWPNIGGFWEGLKYILPSDNK--
FICV      ESLMLNDMITVSDRGLELATVERFNATA-----LGGEKLGGLYFDG---LSSLLPPK--
BoCov     LDPTQLQVANSLMNGVTLSTKLKDGVN-----FNVDINFSPLVG---CLGSACNK--
OC43      LDPTQLQVANSLMNGVTLSTKLKDGVN-----FNVDVNFSPVLG---CLGSECNK--
PHEV      LDPTQLQVANSLMNGVTLSTKLKDGIN-----FNVDINFSPLVG---CLGSECNR--
MHV       LDNMQLQVASALMQVGTISSRLPDGIS-----GPIDDINFSPLLG---CIGSTCAEDG
TOR2_S    QDRNTREVFQAVKQMYKTPTLKYPFGGF-----NFSQILPDPLKP-----
AIBV      EDMELLSFYSSTKPKGYDTPVLSNVSTG-----EFNISLLLTTPSP-----
          . . . . . :

229E      -----VAGRSAIEDILFSKIVTSGLGTVDADYKNCTKGLS--IADLACAQYYNGIMVLP
PEDV      -----VQKRSVIEDLLFNKVVTNGLTGVDEDYKRCNNGRS--VADLVCAQYYSGVMVLP
CCov      -----RKYRSAIEDLLFDKVVTSGLGTVDDEDYKRCSTGGYD--IADLVCAQYYNGIMVLP
PRC       -----RKYRSAIEDLLFSKVVTSGLGTVDDEDYKRCSTGGYD--IADLVCAQYYNGIMVLP
FICV      -----IGKRSAVEDLLFNKVVTSGLGTVDDDYKCCSSGTD--VADLVCAQYYNGIMVLP
BoCov     -----VSSRSAIEDLLFSKVKLSDVG-FVEAYNNCTGGAE--IRDLCVQSYNGIKVLPP
OC43      -----VSSRSAIEDLLFSKVRLSDVG-FVEAYNNCTGGAG--IRDLCVQSYNGIKVLPP
PHEV      -----ASTRSAIEDLLFDKVKLSDVG-FVQAYNNCTGGAE--IRDLCVQSYNGIKVLPP
MHV       NGPSAIRGRSAIEDLLFDKVKLSDVG-FVEAYNNCTGGQE--VRDLCVQSFNGIKVLPP
TOR2_S    -----TKRSFIEDLLFNKVTLADAG-FMKQYGECLGDIN--ARDLCAQKFNGLTVLPP
AIBV      -----SGRSFVEDLLFTSVETVGLP-TDAEYKCKTAGPLGTLKDLICAREYNGLLVLP
          * * : * : * : . . . . . * . * . . . * * : : : * * : * *

229E      VDAERMAMYTGSLIGGIALGGLT----SAVSIPFSLAIQARLNLYVALQTDVLQENQKIL
PEDV      VVDAEKLMYSASLIGGMALGGIT----AAAALPFSYAVQARLNLYVALQTDVLQRNQQLL
CCov      VANDDKMAMYTASLAGGITLGLSGG---GAVSIPFAIAVQARLNLYVALQTDVLNKNQQLL
PRC       VANADKMTMYTASLAGGITLGAFFG---GAVSIPFAVAVQARLNLYVALQTDVLNKNQQLL
FICV      VVDGNKMSMYTASLIGGMALGSIT----SAVAVPFAMQVQARLNLYVALQTDVLQENQKIL
BoCov     LLSVNQISGYTLAATSASLFPPLS----AAGVFFYLVNQYRINGIGVTMDVLSQNKLI
OC43      LLSDNQISGYTLAATSANLFPFWS----AAAGVFFYLVNQYRINGIGVTMDVLSQNKLI
PHEV      LLSNQISGYTLAATAASLFPFWT----AAAGVFFYLVNQYRINGIGVTMDVLSQNKLI
MHV       VLSESQISGYTAGATAAAMPFPWT----AAAGVFFYLVNQYRINGIGVTMDVLSQNKMI
TOR2_S    LLTDDMIAAYTAALVSGTATAGWTFGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKQI
AIBV      IITADMQTMYTASLVGAMAFGGIT----SAAAI PFATQIARINHLGIAQSLLMKNQEKI
          : . . . . . * : . . . . . * : * : : * : * : : * : * : :

229E      AASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQN
PEDV      AESFNSAIGNITSASFESVKEAISQTSKGLNTVAHALTKVQEVVNSQGSALNQLTVQLQHN
CCov      ANAFNQAIGNITQAFGKVNDAIHQTSQGLATVAKVLAKVDVNTQGGALSHLTQLQNN
PRC       ASAFNQAIGNITQSFQKVNDAIHQTSRGLTTVAKALAKVDVNTQGGALRHLTQLQNN
FICV      ANAFNNAIGNITLALGKVSNAITTTSDGFNSMASALTKIQSVVNQGGEALSQLTSQLQKN
BoCov     ANAFNNALDAIQEGFDATN-----S-ALVKIQAVVNANAEALNNLLQQLSNR
OC43      ANAFNNALDAIQEGFDATN-----S-ALVKIQAVVNADAEALNNLLQQLSNR
PHEV      ASAFNNALDAIQEGFDATN-----S-ALVKIQAVVNANAEALNNLLQQLSNR
MHV       ASAFNNALGAIQEGFDATN-----S-ALGKIQSVVNANAEALNNLLQQLSNR
TOR2_S    ANQFNKASIQIESLTTTS-----TALGKLDVVNQNAQALNTLVKQLSSN
AIBV      AASFNKAIGHMQEGFRSTS-----LALQQVDVVNQSAILTETMNSLNKN
          * * * : : : . . . . . * : : * * * : : * . * .

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FIGURE 14D

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229E      FQAISSSSIQAIYDRDLTIQADQQVDRLITGRLAALNVFVSHTLTKEYTEVRASRQLAQQKV
PEDV      FQAISSSIDDIYSRLDILLADVQVDRLITGRLSALNAFVAQTLTKYTEVQASRKLAAQQKV
CCov      FQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRQLAKDKV
PRC       FQAISSSSIQAIYDRDLTIQADQQVDRLITGRLTALNAFVSQTLTRQAEVRASRQLAKDKV
FICV      FQAISSSIAEIYNRLKVEADAQVDRLITGRLAALNAYVSQTLTQYAEVKASRQIALEKV
BoCov     FGAISSSSLQEILSRDLDALEAQAQIDRLINGRLTALNVVVSQQLSDSTLVKFSAAQAMEKV
OC43      FGAISSSSLQEILSRDLDALEAQAQIDRLINGRLTALDAYVSQQLSDSTLVKFSAAQAMEKV
PHEV      FGAISASLQEILSRDLDALEAKAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAEKV
MHV       FGAISASLQEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAEKV
TOR2_S    FGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAETIRASANLAATKM
AIBV      >      FGAISSVIQDIYAQLDAIQADAQVDRLITGRLSLSVLAQSAKQSEYIRVSQQRELATQKI
                * * * * : * : * : * . * : * * * * * : * . : * * * :

229E      NECVKQSQSKRYGFCG-NGTHIFSIVNAAPEGLVFLHTVLLPTQYKDVEAWSGLCV-DG--
PEDV      NECVKQSQSQRYGFCGGDGEHIFSLVQAAPQGLLFLHTVLPVPGDFVNVLAAGLCV-NG--
CCov      NECVRSQSQRFGFCG-NGTHLFLSLANAAPNGMIFFFHTVLLPTAYETVTAWSGICADGDR
PRC       NECVRSQSQRFGFCG-NGTHLFLSLANAAPNGMIFFFHTVLLPTAYETVTAWSGICALDGDR
FICV      NECVKQSQSNRYGFCG-NGTHLFLSLVNSAPEGLLFFHTVLLPTWEVEVTAWSGICVNDT--
BoCov     NECVKQSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCI-----
OC43      NECVKQSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCI-----
PHEV      NECVKQSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCI-----
MHV       NECVKSQTTTRINFCG-NGNHIISLVQNAPYGLCFIHFYSVPTSFKTANVSPGLCI-----
TOR2_S    SECVLGQSKRVDFCG-KGYHLMSPQQAAPHGVFLHVTVPSQERNFTTAPAICH-----
AIBV      >      NECVKQSQSNRYGFCG-SGRHVLISIPQNA PNGIVFIHFTYTPETFNVTIAIVGFCVNPLNA
                . * * * . * : * * * : * * * : * * * : * * * : * * * :

229E      TNGYVLRQPNLALYK-----EGNYYRITSRIMFEPRIPTMADFVQIENCNVTFVNISRS
PEDV      EIALTLREPLVLFTHELQTYTATEYFVSSRRMFEPKPTVSDVQIESCVVTVYNLTSD
CCov      TFGLVVKDQVLTFLRN-----LDDKFYLTPTMTYQPIVATSSDFVQIEGCDVLFVNATVI
PRC       TFGLVVKDQVLTFLRN-----LDDKFYLTPTMTYQPRVATSSDFVQIEGCDVLFVNATVI
FICV      -YAYVLKDFDHSIFS-----YNGTYMVTPRNMFQPRKPQMSDFVQITSCEVTFLNMTYT
BoCov     -AGDRGIAPKSGYFVN-----VNNTWMFTGSGYYYPEPITGNNVVMSTCAVNYTKAPDV
OC43      -AGDRGIAPKSGYFVN-----VNNTWMFTGSGYYYPEPITGNNVVMSTCAVNYTKAPDV
PHEV      -AGDIGISPKSGYFIN-----VNNSWMFTGSSYYYPEPITQNNVVMSTCAVNYTKAPDL
MHV       -SGDRGLAPKAGYFVQ-----DNGEWFKTGSNYYYPEPITDKNSVAMISCAVNYTKAPEV
TOR2_S    -EGKAYFPREGVVFVN-----GTSWFITQRNFFSPQIITDNTFVSGNCDVVGIIINNT
AIBV      >      SQYAIVPANGRGIFIQ-----VNGTYIITSRDMYMPRDI TAGDIVTLTSCQANYVNVNKT
                : : : * : . * .

229E      ELQTIVP-EYIDVNKTLQELSYKL-PNYTVPDLV---VEQYNQTLNLTSEISTLENKSA
PEDV      QLPDVIP-DYIDVNKTLDEILASL-PNRTGPSLP---LDVFNATYLNLTGEIADLEQRSE
CCov      DLPSIIP-DYIDINQTVQDILENFRPNWTVPELP---LDIFNATYLNLTGEINDLEFRSE
PRC       DLPSIIP-DYIDINQTVQDILENFRPNWTVPELT---LDVFNATYLNLTGEIDDLFRSE
FICV      TFQEI VI-DYIDINKTIADMLEQYNPNYTPPELNL-LLDIFNQTKLNLTAEIDQLEQRAD
BoCov     MLNISTP-NLHDFKEELDQWFKNQ--TSVAPDLSL-DY--INVTFLDLQDEMNI-----
OC43      MLNISTP-NLPDFKEELDQWFKNQ--TLVAPDLSL-DY--INVTFLDLQDEMNI-----
PHEV      MLNISTP-NLPDFKEELYQWFKNQ--SSVAPDLSL-DY--INVTFLDLQDEMNI-----
MHV       FLNNSIP-NLPDFKEELDKWFKNQ--TSIAPDLSL-DFEKLNVTFDLTYEMNI-----
TOR2_S    VYDPLQP-ELDSFKEELDQWFKNH---TSPDVLGDISGINASVUNI QKEID-----
AIBV      >      VITTFVEDDDDFNFDDELSKWWDNT--KHGLPDFD---DFNYTVPILNISGEID-----
                : . . . . . * . . . . : * :

229E      ELNVTQKQLQTLIDNINSTLVDLKWLNRVETIYKWPWWVWLCISVVLIFVVSMLLLCCCS
PEDV      SLRNTTEELRSLINNINNTLVLEWLNRVETIYKWPWWVWLIIVIVLIFVVSLLVFCIS
CCov      KLHNTTVELAILIDNINNTLVNLEWLNRIETIYKWPWYVWLLIGLVVIFCIPILLFCCCS
PRC       KLHNTTVELAILIDNINNTLVNLEWLNRIETIYKWPWYVWLLIGLVVIFCIPILLFCCCS
FICV      NLTTIAHELQQYIDNINNTLVLDLWLNRIETIYKWPWYVWLLIGLVVIFCIPILLFCCCS
BoCov     -----RLQEAIKVLNQSYINLKDIGTYEYVYKWPWYVWLLIGFAGVAMLVLLFFICCC
OC43      -----RLQEAIKVLNQSYINLKDIGTYEYVYKWPWYVWLLIGFAGVAMLVLLFFICCC
PHEV      -----RLQEAIKVLNQSYINLKDIGTYEYVYKWPWYVWLLIGLAGVAMLVLLFFICCC
MHV       -----RIQDAIKKLNESYINLKKEVGTIYEMVYKWPWYVWLLIGLAGVAVCVLLFFICCC
TOR2_S    -----RLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMTILLCCM
AIBV      >      -----NIQGVIQGLNDSLINLEELSIIKTYIKWPWYVWLAIGFAIIFILILGWVFFM
                . : . : * : : * . : : * : * * * : * * * : : :

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FIGURE 14E

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229E      TGCCG-FFSCFASSIRGCCSTKL-PYYDVEKIHQ-----
PEDV      TGCCG-CCGCCGACFSGCCRGPRLOPYEAFEKVHVQ-----
CCov      TGCCG-CIGCLGSCCHSICSRRQFESYEPIEKVHVH-----
PRC       TGCCG-CIGCLGSCCHSIFSRRQFENYEPIEKVHVH-----
FICV      TGFCG-CFGCVGSCCHSLCSRRQFETYEPYIEKVHIH-----
BoCov     TGCGTSCFKICGGCCD-DYTGHQELVIK---TSHDD-----
OC43      TGCGTSCFKKCGGCCD-DYTGHQELVIK---TSHEG-----
PHEV      TGCGTSCFKKCGGCCD-DYTGHQEFVIK---TSHDD-----
MHV       TGCGSCCFRKCSCCD-EYGGHQDSIVIHNSAHED-----
TOR2_S    TSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT-----
AIBV      >      TGCCGCCGCGFGIIPLISKCGKKSSYYTTFDNDVVTEQYRPKKSV
          *      .

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Key	Name	Genbank	% ID*
229E	spike glycoprotein [Human coronavirus 229E].	AAK32191	28.6% (SEQ ID NO: 53)
AIBV	spike glycoprotein [Avian infectious bronchitis virus].	AAO34396	27.6% (SEQ ID NO: 54)
BoCov	E2 glycoprotein precursor (Spike glycoprotein)	P25193	30.5% (SEQ ID NO: 55)
CCoV	spike protein - canine coronavirus	S41453	26.1% (SEQ ID NO: 56)
FICV	peplomer protein [Feline infectious peritonitis virus].	BAA06805	25.4% (SEQ ID NO: 57)
MHV	E2 glycoprotein precursor (Spike glycoprotein)	P11225	31.9% (SEQ ID NO: 58)
OC43	surface protein - human coronavirus	S44241	30.7% (SEQ ID NO: 59)
PEDV	spike protein [Porcine epidemic diarrhea virus].	CAA80971	26.0% (SEQ ID NO: 60)
PHEV	spike glycoprotein [porcine hemagglutinating encephalomyelitis virus]	AAL80031	30.5% (SEQ ID NO: 61)
PRC	S protein [Porcine respiratory coronavirus].	AAA46905	27.5% (SEQ ID NO: 62)
TOR2_S	Sars associated virus S glycoprotein (SEQ ID NO: 33)		

FIGURE 14F

```
10      20      30      40      50
TOR2_E  MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVS LVKPTV
      :  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
PGV  MTFPRALTVIDDNG-MVINIIFWFLLIILILLSIALLNIIKLCMVCCNLGRTVVIIVPAQ
      10      20      30      40      50

      60      70
TOR2_E YVYSRVKNLNSSEGVPDLLV (SEQ ID NO: 35)
      ::  ::
PGV  HAYDAYKNFMRIKAYNPDGALLA (SEQ ID NO: 63)
      60      70      80
```

FIGURE 15

MESLVLGVNEKTHVQLSLPVLQVRDVLVRGFGDSVEEALSEAREHLKNGT
 CGLVELEKGVLPQLEQPYVFIKRS DALSTNHGHKVV ELVAEMDGIQYGRS
 GTTLGLVLPVHVGETPIAYRNVLRLKNGKAGGHSYGIDLKSYDLGDELG
 TDPFIEDYEQNWNTKHGSGALRELTRELNGGAVTRYVDNNFCGPDGYPLDC
 IKDFLARAGKSMCTLSEQLDYIESKRGVYCCRDHEHEIAWFTERSDKSYE
 HQTPFEIKSAKKFDTFKGECPKFVFLNSKVKVIQPRVEKKKTEGFMGRI
 RSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFLKATCEHCGTENLV
 IEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHSNIETRLRKG
 GRTRCFGGCVFAYVGCYNKRAYWVPRASADIGSGHTGITGDNVETLNEDL
 LETLSRERVNINIVGDFHLNEEVAILASFSASTSAFIDTILSLDYKSFK
 TIVESCNGYKVTGKPKVGAWNIGQQRSVLTPLCGFPSQAAGVIRSIFAR
 TLDAANHSPDLQRAAVTILDGISEQSLRLVDAMVYTSDDL'TNSVIIMAY
 VTGGLVQQT SQWLSNLLGT'TVEKLRPIFEWIEAKLSAGVEFLKDAWEILK
 FLITGVFDIVKGGQIQVASDNIKDCVKCFIDVVNKALEM CIDQVTIAGAKL
 RSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPLKAPKEVTFLEGDSHDTV
 LTSEEVVLKNGELEALETPVDSFTNGAIVGTPVCVNGLMLEIKDKEQYC
 ALSPGLLATNNVFRLLKGGAPIKGVTFGEDTVWEVQGYKNVRITFELDERV
 DKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLPVSDLLTNMGIDLDE
 WSVATFYFLFDDAGEENFSSRMYCSFYPPDEEEEDDAECEEEDIDETCEHE
 YGTEDDYQGLPLEFGASAE'TVRVEEEEDWLDOTTQESEIEPEPEPTPE
 EPVNOFTGYLKLTDNVAIKCVDIVKEAQSANPMVIVNAANIHLKHGGGVA
 GAINKATNGAMQKESDDYIKLNGPLTVGGSCLLSGHNLAKKCLHVVGNL
 NAGEDIQLLKAAYENFNSQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQ
 VYTAVNDKALYEQVVM DYLDNLKPRVEAPKQEEPNTEDSKTEESVQK
 PVDVKPKIKACIDEVTTTLEETKFLTNKLLLFADINGKLYHDSQNM LRGE
 DMSFLEKDAPYMGVDVITS GDITCVVIPS KAGGTTEMLSRALKKVPVDE
 YIT'TYPGQCAGYTLBEAKTALKKCKSAFYVLPSEAPNAKEEILGTVSN
 LREMLAHAEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIVDYGVRRFF
 YTSKEPVASIIITKLSNLEPLVTMPIGYVTHGFNLEEAARCMRSLKAPAV
 VSVSPDAVTTYNGYLTSSSKTSEEHFVETVSLAGSYRDWSYSGQRTLG
 VEFLLKRGDKIVYHTLESPEVEFHLGDGEVLSLDKLSLLSLREVKTIKVFTT
 VDNINLHTQLVDMMSMTYGGQFGPTYLDGADVTKIKPHVNHEGKTF FVLPS
 DDTLRSEAFEYYHTLDESFLGRYMSALNHTKKWKFPQVGG LTSIKWADNN
 CYLSSVLLALQQLLEVKNAPALQEAYYRARAGDAANFCALILAYSNKTVG
 ELGDVRETMT HLLQHANLES AKRVLVNVCKHCGQKTTTTLTGVEAVMYMG
 LSYDNLKTGVSI PCVCGRDATQYLVQQESSFVMSAPPAEYK LQQGTFLC
 ANEYTGNYQC GHYTHITAKETLYRIDGAHLTKMSEYKGPVTDV FYKETS
 YTTIKPVSYKLDGVTYTEIEPKLDGYKKDNAYYTEQPIDLVPTQPLPNA
 SFDNFKLTC SNTKFADDL NQMTGFTK PASRELSVTFFPDLNGDVVAIDYR
 HYSASFKKGAKLLHKPIVWHINQAT'TKTFKPN'TWCLRLCWSTKPVDTSN
 SFEVLAVEDTQGM DN LACESQQPTSEEVVENPTIQKEVIECDVKTEVVG
 NVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELSLALGLKTIA
 THGIAAINSVPWSKILAYVKPFLGQAAITTSNCAKRLAQRVFN NYPYVF
 TLLFQLCTFTKSTNSRIRASLPTTI AKNSVKSVAKLCLDAGIN VVKS PKF
 SKLFTIAMWLLLSICLGLSICVTAAFGVLLSNFGAPSYCNVRELYLNS
 SNTVTMDFCESFPCSI CLSGLDSDL SYPALETIQVTISSYKLDLTILGL
 AAEWVLAYMLFTKFFYLLGLSAIMQVFFGYFASHFISNSWLMWFIISIVQ
 MAPVSAMVRMYIFFASFYYIWKSYVHIMDGCTSSCTMMCYKRNRRATRVEC
 TTIIVNGMKRSFYVYANGGRGFCKTHNWNCLNCDTFTCTGSTFISDEVARDL
 SLQFKRPINPTDQSSYIVDSVAVKNGALHLYFDKAGQKTYERHPLSHFVN
 LDNL RANNTKGLSPINVI VFDGKSKCDESASKSASVYYSQLMCQPILLLD
 QALVSDVGDSTEVSVKMFDAVDTFSATFSVPMEK LKALVATAHSELAKG
 VALDGVLTSTFVSAARQGVDTDVDTKDVI ECKLSHHSDEVTGDCSNF
 MLTYNKVENMTPRDLGACIDCNARHINAQVAKSHNVSLIWNVKDYMSLSE
 QLRKQIRSAAKKNNIPFRLTCATTRQVNVNITTKISLKGKIVSTCFKLM
 LKATLLCVLALVCYIVMPVHTLSIHDGYTNEIIGYKAIQDGVTRDIIST
 DDCFANKHAGFDWFSQRGGSYKNDKSCPVAAITTREIGFIVPGLP GTV
 LRAINGDFLHFLPRVFSAVGNICYTPSKLIEYSDFATSACVLAECTIFK
 DAMGKPVPCYD TNLLSGSISYSELRPDTRYVLM DGSIIQFPNTYLEGSV
 RVVTTFDAEYCRHGTCERSEVGICLSTSGRWVLNNEHYRALSGVFCGVDA
 MNLIANIFTPLVQPVGALDVSASVAGGIIAILVTCAAYFMKFRRVFGE
 YNHVVAANALLFLMSFTILCLVPAYSFLPGVYSVFYLYLTFYFTNDVSFL
 AHLQWFAMFSPIVPFWITAIYVFCISLKHCHWFFNNYLRKRVMFNGVTFS
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 AVINGDRWFLNRFTTTLNDFNLVAMKYNIEPLTQDHVDILGPLSAQTGIA
 VLDMAALKE LLQNGMNGRTILGSTILEDEFTPFDDVVRQCSGVTFQ GKFK

FIGURE 16A

KIVKGTHHWMLTFLTSLLLLVQSTQWSLFFFVYENAFLEPFTLGIMAIAA
CAMLVLVKKHKAFLCLFLLPSLATVAYFNMVYMPASWVMRIMTWLELADTS
LSGYRLKDCVMYASALVLLIILMTARTVYDDAARRVWTLMNVITLVYKVYY
GNALDQAI SMWALVISVTSNYSGVVTTIMFLARAI VFVCVEYYPLLFITG
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NSQGLLPPKSSIDAFKLNKLLGIGGKPCIKVATVQSKMSDVKCTSVVLL
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AVDINRLCEEMLDNRATLQAIASEFSSLSYAAAYATAQEAYEQAVANGDS
EVLKLLKSLNVAKSEFDRDAAMQRKLEKMAQAMTQMYQARSEDKRA
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VPDYGTYNKTCGNTFTYASALWEIQVVDADSKIVQLSEINMDNSPNLA
WPLIVTALRANSVAVKLQNNELSPVALRQMSCAAGTTQTACTDDNALAYYN
NSKGGRFVLALLSDHQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGP
KVYLYFIKGLNNLNRGMVLGSLAATVRLQAGNATEVPANSTVLSFCAFA
VDPKAYKYDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQESFGG
ASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLRLNTVCTVC
GMWKGYGCSCDQLREPLMQSADASTF

{SEQ ID NO: 64}

FIGURE 16B

FKRVCG
VSAARLTPCGTGTSTDVYRAFDIYNEKVAGFAKFLKTNCCRFOEKDEEG
NLLDSYFVVKRHTMSNYQHEETIYNLVKDCPAVAVHDFFKFRVDGDMVPH
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AVMSLKENQINDMIYSLLEKGRLLIIRENNRVVSSDILVNN

(SEQ ID NO: 65)

FIGURE 17

MDLFMRFFTLRSITAQPVKIDNASPASTVHATATIPLQASLPFGWLVIGV
AFLAVFQSATKIIALNKRWQLALYKGFQFICNLLLLFVTIYSHLLLVAAG
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SSGVANPAMDPIYDEPTTTTTSVPL (SEQ ID NO: 66)

FIGURE 18

MMPTTLFAGTHITMTTVYHITVSQIQLSLLKVTAFOHQNSKKTTKLVVIL
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RMCKYTQSTALQELLIQQWIQFMMSRRRLACLCKHKKVSTNLCTHSFRK
KQVR (SEQ ID NO: 67)

FIGURE 19

MFHLVDFQVTIAEILIIIMRTFRIAIWNLDVIISSIVRQLFKPLTKKNYS
ELDDEEPMELDYP (SEQ ID NO: 68)

FIGURE 20

MKIILFLTILIVFTSCELYHYQECVRGTTVLLKEPCPSGTYEGNSPFHPLA
DNKFALTCTSTHFAFACADGTRHTYQLRARSVSPKLFIRQEEVQQELYSP
LFLIVAALVFLILCFTIKRKTE (SEQ ID NO: 69)

FIGURE 21

MNELTLIDFYLCFLAFLFLVLIMLIIFWFSLEIQDLEEPCTKV
(SEQ ID NO: 70)

FIGURE 22

MKLLIVLTCISLCSCTVQRCASNKPHVLEDPCKVQH
(SEQ ID NO: 71)

FIGURE 23

MCLKILVRYNTRGNTYSTAWLCALGKVLFPHRWHTMVQTCTPNVTINCQD
PAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN (SEQ ID NO: 72)

FIGURE 24

MDPNQTNVVPPALHLVDPQIQLTITRMEAMGQGQNSADPKVYPILRLG
SQLSLSMARRNLDSEARAFQSTPIVVQMTKLATTEELPDEFVVVTAK

(SEQ ID NO: 73)

FIGURE 25

MLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVAVIQEIQLLA AVG
EILLLEWLAEVVKLPSRYCC (SEQ ID NO: 74)

FIGURE 26

CIAVGQLCVFWNIGRPCCSGLCVFA--CTVKL	conotoxin
CISLCS-CICTVVQRCASNKPHVLEDPCKVQH	sars
**::. *: : * ... *: *.*:	

FIGURE 27

SEQUENCE LISTING

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<130> 82936-7

<160> 206

<170> PatentIn version 3.3

<210> 1

<211> 29736

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 1

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 aagaggaggt tcaacaagag ctctactcgc cactttttct cattgttgcgt gctctagtat 27600

ttttaataact ttgcttcacc attaagagaa agacagaatg aatgagctca ctittaattga 27660
 ctctatatttg tgcttttttag cttttctgct attccttggt ttaataatgc ttattatatt 27720
 ttggtttttca ctcgaaatcc aggatctaga agaaccttgt accaaagtct aaacgaacat 27780
 gaaacttctc attgttttga cttgtatttc tctatgcagt tgcatatgca ctgtagtaca 27840
 gcgctgtgca tctaataaac ctcatgtgct tgaagatcct tgtaaggtag aacactaggg 27900
 gtaataactta tagcactgct tggctttgtg ctctaggaaa ggttttacct ttccatagat 27960
 ggcacactat ggttcaaaca tgcacaccta atgttactat caactgtcaa gatccagctg 28020
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 gagacgtact tgttgtttta aataaacgaa caaattaaaa tgtctgataa tggaccccaa 28140
 tcaaaccaac gtagtgcccc ccgcattaca tttggtggac ccacagattc aactgacaat 28200
 aaccagaatg gaggacgcaa tggggcaagg ccaaaacagc gccgaccoca aggtttaccc 28260
 aataatactg cgtcttggtt cacagctctc actcagcatg gcaaggagga acttagattc 28320
 cctcgaggcc agggcgttcc aatcaacacc aatagtggtc cagatgacca aattggctac 28380
 taccgaagag ctaccgacg agttcgtggt ggtgacggca aaatgaaaga gctcagcccc 28440
 agatggtaact tctattacct aggaactggc ccagaagctt cacttcoccta cggcgctaac 28500
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 tcatcacgta gtcgcggtaa ttcaagaaat tcaactcctg gcagcagtag gggaaattct 28740
 cctgctcgaa tggctagcgg aggtggtgaa actgccctcg cgctattgct gctagacaga 28800
 ttgaaccagc ttgagagcaa agtttctggt aaaggccaac aacaacaagg ccaaactgtc 28860
 actaagaaat ctgctgctga ggcatctaaa aagcctcgcc aaaaaogtac tgccacaaaa 28920
 cagtacaacg tcaactcaagc atttgggaga cgtggtccag aacaaaccca aggaaatttc 28980
 ggggaccaag acctaatacag acaaggaact gattacaaac attggccgca aattgcacaa 29040
 tttgctccaa gtgcctctgc attcttttga atgtcacgca ttggcatgga agtcacacct 29100
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 aaagacaacg tcatactgct gaacaagcac attgacgcat acaaaacatt ccaccaaca 29220
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 aagaagcagc ccaactgtgac tcttcttctc gcggctgaca tggatgattt ctccagacaa 29340
 cttcaaaaatt ccatgagtgg agcttctgct gattcaactc aggcataaac actcatgatg 29400
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tactcttgtg cagaatgaat tctcgtaact aaacagcaca agtaggttta gttaacttta 29520
 atctcacata gcaatcttta atcaatgtgt aacattaggg aggacttgaa agagccacca 29580
 cattttcatc gaggccacgc ggagtacgat cgagggtaca gtgaataatg ctagggagag 29640
 ctgcctatat ggaagagccc taatgtgtaa aattaatttt agtagtgcta tccccatgtg 29700
 attttaatag cttcttagga gaatgacaaa aaaaaaaaaa aaaaaaaaaa a 29751

<210> 16
 <211> 47
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 16
 acattttcat cgaggccacg cggagtacga tcgagggtac agtgaat 47

<210> 17
 <211> 32
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 17
 cgaggccacg cggagtacga tcgagggtac ag 32

<210> 18
 <211> 339
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 18
 acactcatga tgaccacaca aggcatatgg gctatgtaaa cgttttcgca attccgttta 60
 cgatacatag tctactcttg tgcagaatga attctcgtaa ctaaacagca caagtaggtt 120
 tagttaactt taatctcaca tagcaatctt taatcaatgt gtaacattag ggaggacttg 180
 aaagagccac cacattttca tcgaggccac gcggagtacg atcgagggtta cagtgaataa 240
 tgctagggag agctgcctat atggaagagc cctaattgtgt aaaattaatt ttagtagtgc 300
 tatcccatg tgattttaat agcttcttag gagaatgac 339

<210> 19
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> s2m motif

<220>
 <221> misc_feature
 <222> (5)..(5)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (23)..(23)

<223> n is a, c, g, or t

<400> 19

gccgnggcc cgcsgagtas gancgagggt acags

35

<210> 20

<211> 26

<212> RNA

<213> Severe acute respiratory syndrome virus

<400> 20

ucucuaaacg aacuuuaaaa ucugug

26

<210> 21

<211> 16

<212> RNA

<213> Severe acute respiratory syndrome virus

<400> 21

caacuaaacg aacaug

16

<210> 22

<211> 18

<212> RNA

<213> Severe acute respiratory syndrome virus

<400> 22

cacuaaacg aacuaug

18

<210> 23

<211> 16

<212> RNA

<213> Severe acute respiratory syndrome virus

<400> 23

ugaguacgaa cuuaug

16

<210> 24

<211> 18

<212> RNA

<213> Severe acute respiratory syndrome virus

<400> 24

ggucuaaacg aacuaacu

18

<210> 25

<211> 11

<212> RNA

<213> Severe acute respiratory syndrome virus

<400> 25
 aacuaaiaaaau u 11

<210> 26
 <211> 17
 <212> RNA
 <213> Severe acute respiratory syndrome virus

<400> 26
 uccauaaaaac gaacaug 17

<210> 27
 <211> 24
 <212> RNA
 <213> Severe acute respiratory syndrome virus

<400> 27
 ugcucuagua uuuuuuauac uuug 24

<210> 28
 <211> 16
 <212> RNA
 <213> Severe acute respiratory syndrome virus

<400> 28
 agucuaaacg aacaug 16

<210> 29
 <211> 15
 <212> RNA
 <213> Severe acute respiratory syndrome virus

<400> 29
 cuaaauaac ucaug 15

<210> 30
 <211> 24
 <212> RNA
 <213> Severe acute respiratory syndrome virus

<400> 30
 uaaauaaacg aacaaauuaa aaug 24

<210> 31
 <211> 136
 <212> DNA
 <213> Equine rhinovirus

<400> 31
 accggttacc ctaaaattcc ctcccctttc tcttcactcg ccgaggccac gccgagtagg 60
 accgagggta cagcgagtct tttagtttaa ggtgttagat gtaagggtacg tgggctttct 120
 tttggtttac ttcttc 136

<210> 32
 <211> 178
 <212> DNA
 <213> Avian infectious bronchitis

<400> 32
 tagtttagtt taagtttagtt tagagtaggt ataaagatgc cagtgccggg gccacgcgga 60
 gtacgatcga gggtagacga ctaggacgcc cattagggga agagctaaat tttagtttaa 120
 gttaagttaa attggctaag tatagttaaa atttataggc tagtatagag ttagagca 178

<210> 33
 <211> 1255
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 33

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
 1 5 10 15

Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
 20 25 30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
 35 40 45

Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
 50 55 60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
 65 70 75 80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
 85 90 95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
 100 105 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
 115 120 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
 130 135 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
 145 150 155 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225 230 235 240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
245 250 255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
260 265 270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
275 280 285

Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
290 295 300

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305 310 315 320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
325 330 335

Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
340 345 350

Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
355 360 365

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370 375 380

Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385 390 395 400

Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe

405 410 415
 Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
 420 425 430
 Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
 435 440 445
 Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
 450 455 460
 Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
 465 470 475 480
 Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
 485 490 495
 Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
 500 505 510
 Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
 515 520 525
 Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
 530 535 540
 Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
 545 550 555 560
 Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
 565 570 575
 Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
 580 585 590
 Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
 595 600 605
 Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
 610 615 620
 Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
 625 630 635 640
 His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
 645 650 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
 660 665 670
 Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
 675 680 685
 Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
 690 695 700
 Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
 705 710 715 720
 Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
 725 730 735
 Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
 740 745 750
 Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
 755 760 765
 Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
 770 775 780
 Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
 785 790 795 800
 Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
 805 810 815
 Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
 820 825 830
 Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
 835 840 845
 Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
 850 855 860
 Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
 865 870 875 880
 Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
 885 890 895

Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
 900 905 910

Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
 915 920 925

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
 930 935 940

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
 945 950 955 960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
 965 970 975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
 980 985 990

Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
 995 1000 1005

Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
 1010 1015 1020

Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
 1025 1030 1035

Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
 1040 1045 1050

Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
 1055 1060 1065

Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
 1070 1075 1080

Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
 1085 1090 1095

Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
 1100 1105 1110

Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
 1115 1120 1125

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
1130 1135 1140

Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
1145 1150 1155

Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
1160 1165 1170

Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
1175 1180 1185

Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu Gly Phe Ile
1190 1195 1200

Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu Cys Cys
1205 1210 1215

Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
1220 1225 1230

Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
1235 1240 1245

Gly Val Lys Leu His Tyr Thr
1250 1255

<210> 34

<211> 220

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 34

Met Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu
1 5 10 15

Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
20 25 30

Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
35 40 45

Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
50 55 60

Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
65 70 75 80

Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
85 90 95

Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
100 105 110

Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
115 120 125

Thr Arg Pro Leu Met Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile
130 135 140

Arg Gly His Leu Arg Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile
145 150 155 160

Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
165 170 175

Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
180 185 190

Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
195 200 205

His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val
210 215 220

<210> 35

<211> 76

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 35

Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
1 5 10 15

Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
20 25 30

Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
35 40 45

Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
50 55 60

Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
65 70 75

<210> 36
<211> 422
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 36

Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
1 5 10 15

Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
20 25 30

Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
35 40 45

Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
50 55 60

Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
65 70 75 80

Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
85 90 95

Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
100 105 110

Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
115 120 125

Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
130 135 140

Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
145 150 155 160

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
165 170 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
180 185 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
195 200 205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
 210 215 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
 225 230 235 240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
 245 250 255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
 260 265 270

Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
 275 280 285

Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
 290 295 300

Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg
 305 310 315 320

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
 325 330 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
 340 345 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
 355 360 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
 370 375 380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
 385 390 395 400

Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
 405 410 415

Ala Asp Ser Thr Gln Ala
 420

<210> 37
 <211> 230
 <212> PRT

<213> Bovine coronavirus

<400> 37

Met Ser Ser Val Thr Thr Pro Ala Pro Val Tyr Thr Trp Thr Ala Asp
 1 5 10 15

Glu Ala Ile Lys Phe Leu Lys Glu Trp Asn Phe Ser Leu Gly Ile Ile
 20 25 30

Leu Leu Phe Ile Thr Val Ile Leu Gln Phe Gly Tyr Thr Ser Arg Ser
 35 40 45

Met Phe Val Tyr Val Ile Lys Met Val Ile Leu Trp Leu Met Trp Pro
 50 55 60

Leu Thr Ile Ile Leu Thr Ile Phe Asn Cys Val Tyr Ala Leu Asn Asn
 65 70 75 80

Val Tyr Leu Gly Phe Ser Ile Val Phe Thr Ile Val Ala Ile Ile Met
 85 90 95

Trp Ile Val Tyr Phe Val Asn Ser Ile Arg Leu Phe Ile Arg Thr Gly
 100 105 110

Ser Trp Trp Ser Phe Asn Pro Glu Thr Asn Asn Leu Met Cys Ile Asp
 115 120 125

Met Lys Gly Arg Met Tyr Val Arg Pro Ile Ile Glu Asp Tyr His Thr
 130 135 140

Leu Thr Val Thr Ile Ile Arg Gly His Leu Tyr Met Gln Gly Ile Lys
 145 150 155 160

Leu Gly Thr Gly Tyr Ser Leu Ser Asp Leu Pro Ala Tyr Val Thr Val
 165 170 175

Ala Lys Val Ser His Leu Leu Thr Tyr Lys Arg Gly Phe Leu Asp Lys
 180 185 190

Ile Gly Asp Thr Ser Gly Phe Ala Val Tyr Val Lys Ser Lys Val Gly
 195 200 205

Asn Tyr Arg Leu Pro Ser Thr Gln Lys Gly Ser Gly Leu Asp Thr Ala
 210 215 220

Leu Leu Arg Asn Asn Ile

225

230

<210> 38
 <211> 226
 <212> PRT
 <213> Avian infectious bronchitis virus

<400> 38

Met Ser Asn Gly Thr Glu Asn Cys Thr Leu Ser Thr Gln Gln Ala Ala
 1 5 10 15

Glu Leu Phe Lys Glu Tyr Asn Leu Phe Ile Thr Ala Phe Leu Leu Phe
 20 25 30

Leu Thr Ile Leu Leu Gln Tyr Gly Tyr Ala Thr Arg Ser Arg Phe Ile
 35 40 45

Tyr Ile Leu Lys Met Ile Val Leu Trp Cys Phe Trp Pro Leu Asn Ile
 50 55 60

Ala Val Gly Ile Ile Ser Cys Ile Tyr Pro Pro Asn Thr Gly Gly Leu
 65 70 75 80

Val Ala Ala Ile Ile Leu Thr Val Phe Ala Cys Leu Ser Phe Val Gly
 85 90 95

Tyr Trp Ile Gln Ser Phe Arg Leu Phe Lys Arg Cys Arg Ser Trp Trp
 100 105 110

Ser Phe Asn Pro Glu Ser Asn Ala Val Gly Ser Ile Leu Leu Thr Asn
 115 120 125

Gly Gln Gln Cys Asn Phe Ala Ile Glu Ser Val Pro Met Val Leu Ser
 130 135 140

Pro Ile Ile Lys Asn Gly Ala Leu Tyr Cys Glu Gly Gln Trp Leu Ala
 145 150 155 160

Lys Cys Glu Pro Asp His Leu Pro Lys Asp Ile Phe Val Cys Thr Pro
 165 170 175

Asp Arg Arg Asn Ile Tyr Arg Met Val Gln Lys Tyr Thr Gly Asp Gln
 180 185 190

Ser Gly Asn Lys Lys Arg Phe Ala Thr Phe Val Tyr Ala Lys Gln Ser
 195 200 205

Val Asp Thr Gly Glu Leu Gly Ser Val Ala Thr Gly Gly Ser Ser Leu
 210 215 220

Tyr Thr
 225

<210> 39
 <211> 262
 <212> PRT
 <213> Transmissible gastroenteritis virus
 <400> 39

Met Lys Ile Leu Leu Ile Leu Ala Cys Val Ile Ala Cys Ala Cys Gly
 1 5 10 15

Glu Arg Tyr Cys Ala Met Lys Ser Asp Thr Asp Leu Ser Cys Arg Asn
 20 25 30

Ser Thr Ala Ser Asp Cys Glu Ser Cys Phe Asn Gly Gly Asp Leu Ile
 35 40 45

Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Ile Ile Leu Ile Val
 50 55 60

Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln Phe Ser Trp Phe Val
 65 70 75 80

Tyr Gly Ile Lys Met Leu Ile Met Trp Leu Leu Trp Pro Val Val Leu
 85 90 95

Ala Leu Thr Ile Phe Asn Ala Tyr Ser Glu Tyr Gln Val Ser Arg Tyr
 100 105 110

Val Met Phe Gly Phe Ser Ile Ala Gly Ala Ile Val Thr Phe Val Leu
 115 120 125

Trp Ile Met Tyr Phe Val Arg Ser Ile Gln Leu Tyr Arg Arg Thr Lys
 130 135 140

Ser Trp Trp Ser Phe Asn Pro Glu Thr Lys Ala Ile Leu Cys Val Ser
 145 150 155 160

Ala Leu Gly Arg Ser Tyr Val Leu Pro Leu Glu Gly Val Pro Thr Gly
 165 170 175

Val Thr Leu Thr Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys

180 185 190

Ile Ala Gly Gly Met Asn Ile Asp Asn Leu Pro Lys Tyr Val Met Val
195 200 205

Ala Leu Pro Ser Arg Thr Ile Val Tyr Thr Leu Val Gly Lys Lys Leu
210 215 220

Lys Ala Ser Ser Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala
225 230 235 240

Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu Gln Glu
245 250 255

Lys Leu Leu His Met Val
260

<210> 40
<211> 263
<212> PRT
<213> feline coronavirus

<400> 40

Met Lys Ile Leu Leu Ile Leu Ala Cys Ala Val Ala Cys Val Tyr Gly
1 5 10 15

Glu Gln Ile Arg Tyr Cys Ala Met Gln Glu Thr Gly Leu Ser Cys Arg
20 25 30

Asn Gly Thr Ala Ser Asp Cys Glu Ser Cys Phe Asn Gly Gly Asp Leu
35 40 45

Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Ile Ile Leu Ile
50 55 60

Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln Phe Ser Trp Phe
65 70 75 80

Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu Leu Trp Pro Ile Val
85 90 95

Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser Glu Tyr Glu Val Ser Arg
100 105 110

Tyr Val Met Phe Gly Phe Ser Val Ala Gly Ala Val Val Thr Phe Ala
115 120 125

Leu Trp Met Met Tyr Phe Val Arg Ser Ile Gln Leu Tyr Arg Arg Thr
130 135 140

Lys Ser Trp Trp Ser Phe Asn Pro Glu Thr Asn Ala Ile Leu Cys Val
145 150 155 160

Asn Ala Leu Gly Arg Ser Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr
165 170 175

Gly Val Thr Leu Thr Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe
180 185 190

Lys Met Ala Gly Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met
195 200 205

Ile Arg Thr Pro Asn Arg Thr Ile Val Tyr Thr Leu Val Gly Lys Gln
210 215 220

Leu Lys Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys
225 230 235 240

Ala Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His
245 250 255

Glu Lys Leu Leu His Met Val
260

<210> 41

<211> 231

<212> PRT

<213> Human coronavirus OC43

MSSKTTAPVYIWTADAEAIKFLKEWNFSLGIILLFITIILQFGYTSRSMFVYVIKMIILWLMWPLTIILTIFNCVY
ALNNVYLGLSIVFTIVAIIMWIVYFVNSIRLFIRTGSFWSFNPETNNLMCIDMKGTMYVRPIEDYHTLTVTIIRG
HLYIQGIKLGTYGYSWADLPAYMTVAKVTHLCTYKRGFLDRISDTSGFAVYVKSKVGNRYRLPSTQKSGGMDTALLRN
NI

<SEQ ID NO:37;prr;Porcine hemagglutinating encephalomyelitis virus

<400> 41

Met Ser Ser Pro Thr Thr Pro Val Pro Val Ile Ser Trp Thr Ala Asp
1 5 10 15

Glu Ala Ile Lys Phe Leu Lys Glu Trp Asn Phe Ser Leu Gly Ile Ile
20 25 30

Val Leu Phe Ile Thr Ile Ile Leu Gln Phe Gly Tyr Thr Ser Arg Ser
35 40 45

Met Phe Val Tyr Val Ile Lys Met Val Ile Leu Trp Leu Met Trp Pro
50 55 60

Leu Thr Ile Ile Leu Thr Ile Phe Asn Cys Val Tyr Ala Leu Asn Asn
65 70 75 80

Val Tyr Leu Gly Phe Ser Ile Val Phe Thr Ile Val Ala Ile Ile Met
85 90 95

Trp Val Val Tyr Phe Val Asn Ser Ile Arg Leu Phe Ile Arg Thr Gly
100 105 110

Ser Trp Trp Ser Phe Asn Pro Glu Thr Asn Asn Leu Met Cys Ile Asp
115 120 125

Met Lys Gly Arg Met Tyr Val Arg Pro Ile Ile Glu Asp Tyr His Thr
130 135 140

Leu Thr Ala Thr Ile Ile Arg Gly His Leu Tyr Ile Gln Gly Ile Lys
145 150 155 160

Leu Gly Thr Gly Tyr Ser Leu Ser Asp Leu Pro Ala Tyr Val Thr Val
165 170 175

Ala Lys Val Thr His Leu Cys Thr Tyr Lys Arg Gly Phe Leu Asp Arg
180 185 190

Ile Gly Asp Thr Ser Gly Phe Ala Val Tyr Val Lys Ser Lys Val Gly
195 200 205

Asn Tyr Arg Leu Pro Ser Thr His Lys Gly Ser Gly Met Asp Thr Ala
210 215 220

Leu Leu Arg Asn Asn Ile Met
225 230

<210> 42

<211> 223

<212> PRT

<213> Avian infectious bronchitis virus

<400> 42

Met Met Glu Asn Cys Thr Leu Asn Leu Glu Gln Ala Thr Leu Leu Phe
1 5 10 15

Lys Glu Tyr Asn Leu Phe Ile Thr Ala Phe Leu Leu Phe Leu Thr Ile

20 25 30
 Leu Leu Gln Tyr Gly Tyr Ala Thr Arg Ser Arg Phe Ile Tyr Ile Leu
 35 40 45
 Lys Met Ile Val Leu Trp Cys Phe Trp Pro Leu Asn Ile Ala Val Gly
 50 55 60
 Val Ile Ser Cys Ile Tyr Pro Pro Asn Thr Gly Gly Leu Val Ala Ala
 65 70 75 80
 Ile Ile Leu Thr Val Phe Ala Cys Leu Ser Phe Val Gly Tyr Trp Ile
 85 90 95
 Gln Ser Cys Arg Leu Phe Lys Arg Cys Arg Ser Trp Trp Ser Phe Asn
 100 105 110
 Pro Glu Ser Asn Ala Val Gly Ser Ile Leu Leu Thr Asn Gly Gln Gln
 115 120 125
 Cys Asn Phe Ala Ile Glu Ser Val Pro Met Val Leu Ala Pro Ile Ile
 130 135 140
 Lys Asn Gly Val Leu Tyr Cys Glu Gly Gln Trp Leu Ala Lys Cys Glu
 145 150 155 160
 Pro Asp His Leu Pro Lys Asp Ile Phe Val Cys Thr Pro Asp Arg Arg
 165 170 175
 Asn Ile Tyr Arg Met Val Gln Lys Tyr Thr Gly Asp Gln Ser Gly Asn
 180 185 190
 Lys Lys Arg Val Ala Thr Phe Val Tyr Ala Lys Gln Ser Val Asp Thr
 195 200 205
 Gly Glu Leu Glu Ser Val Pro Thr Gly Gly Ser Ser Leu Tyr Thr
 210 215 220

 <210> 43
 <211> 455
 <212> PRT
 <213> Mouse Hepatitis Virus

 <400> 43

 Met Ser Phe Val Pro Gly Gln Glu Asn Ala Gly Ser Arg Ser Ser Ser
 1 5 10 15

Val Asn Arg Ala Gly Asn Gly Ile Leu Lys Lys Thr Thr Trp Ala Asp
 20 25 30
 Gln Thr Glu Arg Gly Pro Asn Asn Gln Asn Arg Gly Arg Arg Asn Gln
 35 40 45
 Pro Lys Gln Thr Ala Thr Thr Gln Pro Asn Ser Gly Ser Val Val Pro
 50 55 60
 His Tyr Ser Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu
 65 70 75 80
 Phe Gln Phe Ala Gln Gly Gln Gly Val Pro Ile Ala Asn Gly Ile Pro
 85 90 95
 Ala Ser Glu Gln Lys Gly Tyr Trp Tyr Arg His Asn Arg Arg Ser Phe
 100 105 110
 Lys Thr Pro Asp Gly Gln Gln Lys Gln Leu Leu Pro Arg Trp Tyr Phe
 115 120 125
 Tyr Tyr Leu Gly Thr Gly Pro His Ala Gly Ala Glu Tyr Gly Asp Asp
 130 135 140
 Ile Asp Gly Val Val Trp Val Ala Ser Gln Gln Ala Asp Thr Lys Thr
 145 150 155 160
 Thr Ala Asp Ile Val Glu Arg Asp Pro Ser Ser His Glu Ala Ile Pro
 165 170 175
 Thr Arg Phe Ala Pro Gly Thr Val Leu Pro Gln Gly Phe Tyr Val Glu
 180 185 190
 Gly Ser Gly Arg Ser Ala Pro Ala Ser Arg Ser Gly Ser Arg Ser Gln
 195 200 205
 Ser Arg Gly Pro Asn Asn Arg Ala Arg Ser Ser Ser Asn Gln Arg Gln
 210 215 220
 Pro Ala Ser Thr Val Lys Pro Asp Met Ala Glu Glu Ile Ala Ala Leu
 225 230 235 240
 Val Leu Ala Lys Leu Gly Lys Asp Ala Gly Gln Pro Lys Gln Val Thr
 245 250 255

Lys Gln Ser Ala Lys Glu Val Arg Gln Lys Ile Leu Asn Lys Pro Arg
260 265 270

Gln Lys Arg Thr Pro Asn Lys Gln Cys Pro Val Gln Gln Cys Phe Gly
275 280 285

Lys Arg Gly Pro Asn Gln Asn Phe Gly Gly Ser Glu Met Leu Lys Leu
290 295 300

Gly Thr Ser Asp Pro Gln Phe Pro Ile Leu Ala Glu Leu Ala Pro Thr
305 310 315 320

Pro Ser Ala Phe Phe Phe Gly Ser Lys Leu Glu Leu Val Lys Lys Asn
325 330 335

Ser Gly Gly Ala Asp Asp Pro Thr Lys Asp Val Tyr Glu Leu Gln Tyr
340 345 350

Ser Gly Ala Ile Arg Phe Asp Ser Thr Leu Pro Gly Phe Glu Thr Ile
355 360 365

Met Lys Val Leu Asn Glu Asn Leu Asp Ala Tyr Gln Asp Gln Ala Gly
370 375 380

Gly Ala Asp Val Val Ser Pro Lys Pro Gln Arg Lys Arg Gly Thr Lys
385 390 395 400

Gln Lys Ala Leu Lys Gly Glu Val Asp Asn Val Ser Val Ala Lys Pro
405 410 415

Lys Ser Ser Val Gln Arg Asn Val Ser Arg Glu Leu Thr Pro Glu Asp
420 425 430

Arg Ser Leu Leu Ala Gln Ile Leu Asp Asp Gly Val Val Pro Asp Gly
435 440 445

Leu Glu Asp Asp Ser Asn Val
450 455

<210> 44

<211> 448

<212> PRT

<213> Bovine coronavirus

<400> 44

Met Ser Phe Thr Pro Gly Lys Gln Ser Ser Ser Arg Ala Ser Ser Gly
1 5 10 15

Asn Arg Ser Gly Asn Gly Ile Leu Lys Trp Ala Asp Gln Ser Asp Gln
 20 25 30

Ser Arg Asn Val Gln Thr Arg Gly Arg Arg Ala Gln Pro Lys Gln Thr
 35 40 45

Ala Thr Ser Gln Gln Pro Ser Gly Gly Asn Val Val Pro Tyr Tyr Ser
 50 55 60

Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu Phe Glu Phe
 65 70 75 80

Ala Glu Gly Gln Gly Val Pro Ile Ala Pro Gly Val Pro Ala Thr Glu
 85 90 95

Ala Lys Gly Tyr Trp Tyr Arg His Asn Arg Arg Ser Phe Lys Thr Ala
 100 105 110

Asp Gly Asn Gln Arg Gln Leu Leu Pro Arg Trp Tyr Phe Tyr Tyr Leu
 115 120 125

Gly Thr Gly Pro His Ala Lys Asp Gln Tyr Gly Thr Asp Ile Asp Gly
 130 135 140

Val Tyr Trp Val Ala Ser Asn Gln Ala Asp Val Asn Thr Pro Ala Asp
 145 150 155 160

Ile Leu Asp Arg Asp Pro Ser Ser Asp Glu Ala Ile Pro Thr Arg Phe
 165 170 175

Pro Pro Gly Thr Val Leu Pro Gln Gly Tyr Tyr Ile Glu Gly Ser Gly
 180 185 190

Arg Ser Ala Pro Asn Ser Arg Ser Thr Ser Arg Ala Ser Ser Arg Ala
 195 200 205

Ser Ser Ala Gly Ser Arg Ser Arg Ala Asn Ser Gly Asn Arg Thr Pro
 210 215 220

Thr Ser Gly Val Thr Pro Asp Met Ala Asp Gln Ile Ala Ser Leu Val
 225 230 235 240

Leu Ala Lys Leu Gly Lys Asp Ala Ala Lys Pro Gln Gln Val Thr Lys
 245 250 255

Gln Thr Ala Lys Glu Ile Arg Gln Lys Ile Leu Asn Lys Pro Arg Gln
260 265 270

Lys Arg Ser Pro Asn Lys Gln Cys Thr Val Gln Gln Cys Phe Gly Lys
275 280 285

Arg Gly Pro Asn Gln Asn Phe Gly Gly Gly Glu Met Leu Lys Leu Gly
290 295 300

Thr Ser Asp Pro Gln Phe Pro Ile Leu Ala Glu Leu Ala Pro Thr Ala
305 310 315 320

Gly Ala Phe Phe Phe Gly Ser Arg Leu Glu Leu Ala Lys Val Gln Asn
325 330 335

Leu Ser Gly Asn Leu Asp Glu Pro Gln Lys Asp Val Tyr Glu Leu Arg
340 345 350

Tyr Asn Gly Ala Ile Arg Phe Asp Ser Thr Leu Ser Gly Phe Glu Thr
355 360 365

Ile Met Lys Val Leu Asn Glu Asn Leu Asn Ala Tyr Gln Gln Gln Asp
370 375 380

Gly Thr Met Asn Met Ser Pro Lys Pro Gln Arg Gln Arg Gly Gln Lys
385 390 395 400

Asn Gly Gln Gly Glu Asn Asp Asn Ile Ser Val Ala Ala Pro Lys Ser
405 410 415

Arg Val Gln Gln Asn Lys Ile Arg Glu Leu Thr Ala Glu Asp Ile Ser
420 425 430

Leu Leu Lys Lys Met Asp Glu Pro Phe Thr Glu Asp Thr Ser Glu Ile
435 440 445

<210> 45

<211> 409

<212> PRT

<213> Avian infectious bronchitis virus

<400> 45

Met Ala Ser Gly Lys Ala Ala Gly Lys Thr Asp Ala Pro Ala Pro Val
1 5 10 15

Ile Lys Leu Gly Gly Pro Lys Pro Pro Lys Val Gly Ser Ser Gly Asn

20 25 30
 Ala Ser Trp Phe Gln Ala Leu Lys Ala Lys Lys Leu Asn Ala Pro Ala
 35 40 45
 Pro Lys Phe Glu Gly Ser Gly Val Pro Asp Asn Glu Asn Leu Lys Ile
 50 55 60
 Ser Gln Gln His Gly Tyr Trp Arg Arg Gln Ala Arg Tyr Lys Pro Gly
 65 70 75 80
 Lys Gly Gly Arg Lys Pro Val Pro Asp Ala Trp Tyr Phe Tyr Tyr Thr
 85 90 95
 Gly Thr Gly Pro Ala Ala Asp Leu Asn Trp Gly Asp Ser Gln Asp Gly
 100 105 110
 Ile Val Trp Val Ala Ala Lys Gly Ala Asp Val Lys Ser Arg Ser Asn
 115 120 125
 Gln Gly Thr Arg Asp Pro Asp Lys Phe Asp Gln Tyr Pro Leu Arg Phe
 130 135 140
 Ser Asp Gly Gly Pro Asp Gly Asn Phe Arg Trp Asp Phe Ile Pro Leu
 145 150 155 160
 Asn Arg Gly Arg Ser Gly Arg Ser Thr Ala Ala Ser Ser Ala Ala Ser
 165 170 175
 Ser Arg Ala Pro Ser Arg Glu Gly Ser Arg Gly Arg Leu Asn Gly Ala
 180 185 190
 Glu Asp Asp Leu Ile Ala Arg Ala Ala Lys Ile Ile Gln Asp Gln Gln
 195 200 205
 Lys Lys Gly Ser Arg Ile Thr Lys Ala Lys Ala Glu Glu Met Ile His
 210 215 220
 Arg Arg Tyr Cys Lys Arg Thr Val Pro Pro Gly Val Ser Ile Asp Lys
 225 230 235 240
 Val Phe Gly Pro Arg Thr Lys Gly Lys Glu Gly Asn Phe Gly Asp Asp
 245 250 255
 Lys Met Asn Glu Glu Gly Ile Lys Asp Gly Arg Val Thr Ala Met Leu
 260 265 270

Asn Leu Val Pro Ser Ser His Ala Cys Leu Phe Gly Ser Gln Val Thr
 275 280 285

Pro Lys Leu Gln Pro Asp Gly Leu His Leu Thr Phe Arg Phe Thr Thr
 290 295 300

Val Val Ser Arg Asp Asp Pro Gln Phe Asp Asn Tyr Val Lys Ile Cys
 305 310 315 320

Asp Glu Cys Val Asp Gly Val Gly Thr Arg Pro Lys Asp Glu Val Val
 325 330 335

Arg Pro Lys Ser Arg Ser Ser Ser Arg Pro Ala Thr Arg Gly Thr Ser
 340 345 350

Pro Ala Pro Lys Gln Gln Arg Pro Lys Lys Glu Lys Lys Pro Lys Lys
 355 360 365

Gln Asp Asp Glu Val Asp Lys Ala Leu Thr Ser Asp Glu Glu Arg Asn
 370 375 380

Asn Ala Gln Leu Glu Phe Asp Asp Glu Pro Lys Val Ile Asn Trp Gly
 385 390 395 400

Asp Ser Ala Leu Gly Glu Asn Glu Leu
 405

<210> 46

<211> 376

<212> PRT

<213> Feline coronavirus

<400> 46

Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser Lys
 1 5 10 15

Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp Ile Pro
 20 25 30

Leu Ser Tyr Phe Asn Pro Ile Thr Leu Asp Gln Gly Ser Lys Phe Trp
 35 40 45

Asn Leu Cys Pro Arg Asp Phe Val Pro Lys Gly Ile Gly Asn Lys Asp
 50 55 60

Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ala Arg Tyr Arg Ile Val Lys
65 70 75 80

Gly Gln Arg Val Glu Leu Pro Glu Arg Trp Phe Phe Tyr Phe Leu Gly
85 90 95

Thr Gly Pro His Ala Asp Ala Lys Phe Lys Ala Lys Ile Asp Gly Val
100 105 110

Phe Trp Val Ala Arg Asp Gly Ala Met Asn Lys Pro Thr Ser Leu Gly
115 120 125

Thr Arg Gly Thr Asn Asn Glu Ser Lys Pro Leu Lys Phe Asp Gly Lys
130 135 140

Ile Pro Pro Gln Phe Gln Leu Glu Val Asn Arg Ser Arg Asn Asn Ser
145 150 155 160

Arg Ser Gly Ser Gln Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser
165 170 175

Arg Gly Arg Gln Gln Ser Asn Asn Gln Asn Thr Asn Val Glu Asp Thr
180 185 190

Ile Val Ala Val Leu Gln Lys Leu Gly Val Thr Asp Lys Gln Arg Ser
195 200 205

Arg Ser Lys Ser Gly Glu Arg Ser Gln Ser Lys Ser Arg Asp Thr Thr
210 215 220

Pro Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly
225 230 235 240

Asp Val Thr Asn Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe Gly
245 250 255

Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr Pro Gln
260 265 270

Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Leu Phe Gly Ser Gln
275 280 285

Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val Thr Leu Thr His
290 295 300

Asn Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr Ser Gln Phe Leu Glu

Ser Arg Gly Ala Asn Asn Glu Ser Lys Ala Leu Lys Phe Asp Gly Lys
130 135 140

Val Pro Gly Glu Phe Gln Leu Glu Val Asn Gln Ser Arg Asp Asn Ser
 145 150 155 160

Arg Leu Arg Ser Gln Ser Arg Ser Arg Ser Arg Asn Arg Ser Gln Ser
 165 170 175

Arg Gly Arg Gln Gln Ser Asn Asn Lys Lys Asp Asp Ser Val Glu Gln
 180 185 190

Ala Val Leu Ala Ala Leu Lys Lys Leu Gly Val Tyr Thr Glu Lys Gln
 195 200 205

Gln Gln Arg Ser Arg Ser Lys Ser Lys Glu Arg Ser Asn Ser Lys Ile
 210 215 220

Arg Asp Thr Thr Pro Lys Asn Glu Asn Lys His Thr Trp Lys Arg Thr
 225 230 235 240

Ala Gly Lys Gly Asp Val Thr Arg Phe Tyr Gly Thr Arg Ser Asn Ser
 245 250 255

Ala Asn Phe Gly Asp Ser Asp Leu Val Ala Asn Gly Ser Ser Ala Lys
 260 265 270

His Tyr Pro Gln Leu Ala Glu Cys Val Pro Ser Val Ser Ser Ile Leu
 275 280 285

Phe Gly Ser Tyr Trp Thr Ser Lys Glu Asp Gly Asp Gln Ile Glu Val
 290 295 300

Thr Phe Thr His Lys Tyr His Leu Pro Lys Asp Asp Pro Lys Thr Gly
 305 310 315 320

Gln Phe Leu Gln Gln Ile Asn Ala Tyr Ala Arg Pro Ser Glu Val Ala
 325 330 335

Lys Glu Gln Arg Lys Arg Lys Ser Arg Ser Lys Ser Ala Glu Arg Ser
 340 345 350

Glu Gln Glu Val Val Pro Asp Ala Leu Ile Glu Asn Tyr Thr Asp Val
 355 360 365

Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val Thr Asn
 370 375 380

<210> 48
 <211> 389
 <212> PRT
 <213> Human coronavirus 229E

<400> 48

Met Ala Thr Val Lys Trp Ala Asp Ala Ser Glu Pro Gln Arg Gly Arg
 1 5 10 15

Gln Gly Arg Ile Pro Tyr Ser Leu Tyr Ser Pro Leu Leu Val Asp Ser
 20 25 30

Glu Gln Pro Trp Lys Val Ile Pro Arg Asn Leu Val Pro Ile Asn Lys
 35 40 45

Lys Asp Lys Asn Lys Leu Ile Gly Tyr Trp Asn Val Gln Lys Arg Phe
 50 55 60

Arg Thr Arg Lys Gly Lys Arg Val Asp Leu Ser Pro Lys Leu His Phe
 65 70 75 80

Tyr Tyr Leu Gly Thr Gly Pro His Lys Asp Ala Lys Phe Arg Glu Arg
 85 90 95

Val Glu Gly Val Val Trp Val Ala Val Asp Gly Ala Lys Thr Glu Pro
 100 105 110

Thr Gly Tyr Gly Val Arg Arg Lys Asn Ser Glu Pro Glu Ile Pro His
 115 120 125

Phe Asn Gln Lys Leu Pro Asn Gly Val Thr Val Val Glu Glu Pro Asp
 130 135 140

Ser Arg Ala Pro Ser Arg Ser Gln Ser Arg Ser Gln Ser Arg Gly Arg
 145 150 155 160

Gly Glu Ser Lys Pro Gln Ser Arg Asn Pro Ser Ser Asp Arg Asn His
 165 170 175

Asn Ser Gln Asp Asp Ile Met Lys Ala Val Ala Ala Ala Leu Lys Ser
 180 185 190

Leu Gly Phe Asp Lys Pro Gln Glu Lys Asp Lys Lys Ser Ala Lys Thr
 195 200 205

Gly Thr Pro Lys Pro Ser Arg Asn Gln Ser Pro Ala Ser Ser Gln Thr
 210 215 220

Ser Ala Lys Ser Leu Ala Arg Ser Gln Ser Ser Glu Thr Lys Glu Gln
 225 230 235 240

Lys His Glu Met Gln Lys Pro Arg Trp Lys Arg Gln Pro Asn Asp Asp
 245 250 255

Val Thr Ser Asn Val Thr Gln Cys Phe Gly Pro Arg Asp Leu Asp His
 260 265 270

Asn Phe Gly Ser Ala Gly Val Val Ala Asn Gly Val Lys Ala Lys Gly
 275 280 285

Tyr Pro Gln Phe Ala Glu Leu Val Pro Ser Thr Ala Ala Met Leu Phe
 290 295 300

Asp Ser His Ile Val Ser Lys Glu Ser Gly Asn Thr Val Val Leu Thr
 305 310 315 320

Phe Thr Thr Arg Val Thr Val Pro Lys Asp His Pro His Leu Gly Lys
 325 330 335

Phe Leu Glu Glu Leu Asn Ala Phe Thr Arg Glu Met Gln Gln His Pro
 340 345 350

Leu Leu Asn Pro Ser Ala Leu Glu Phe Asn Pro Ser Gln Thr Ser Pro
 355 360 365

Ala Thr Ala Glu Pro Val Arg Asp Glu Val Ser Ile Glu Thr Asp Ile
 370 375 380

Ile Asp Glu Val Asn
 385

<210> 49
 <211> 448
 <212> PRT
 <213> Human coronavirus

<400> 49

Met Ser Phe Thr Pro Gly Lys Gln Ser Ser Ser Arg Ala Ser Ser Gly
 1 5 10 15

Asn Arg Ser Gly Asn Gly Ile Leu Lys Trp Ala Asp Gln Ser Asp Gln
 20 25 30

Val Arg Asn Val Gln Thr Arg Gly Arg Arg Ala Gln Pro Lys Gln Thr
 35 40 45
 Ala Thr Ser Gln Gln Pro Ser Gly Gly Asn Val Val Pro Tyr Tyr Ser
 50 55 60
 Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu Phe Glu Phe
 65 70 75 80
 Val Glu Gly Gln Gly Pro Pro Ile Ala Pro Gly Val Pro Ala Thr Glu
 85 90 95
 Ala Lys Gly Tyr Trp Tyr Arg His Asn Arg Gly Ser Phe Lys Thr Ala
 100 105 110
 Asp Gly Asn Gln Arg Gln Leu Leu Pro Arg Trp Tyr Phe Tyr Tyr Leu
 115 120 125
 Gly Thr Gly Pro His Ala Lys Asp Gln Tyr Gly Thr Asp Ile Asp Gly
 130 135 140
 Val Tyr Trp Val Ala Ser Asn Gln Ala Asp Val Asn Thr Pro Ala Asp
 145 150 155 160
 Ile Val Asp Arg Asp Pro Ser Ser Asp Glu Ala Ile Pro Thr Arg Phe
 165 170 175
 Pro Pro Gly Thr Val Leu Pro Gln Gly Tyr Tyr Ile Glu Gly Ser Gly
 180 185 190
 Arg Ser Ala Pro Asn Ser Arg Ser Thr Ser Arg Thr Ser Ser Arg Ala
 195 200 205
 Ser Ser Ala Gly Ser Arg Ser Arg Ala Asn Ser Gly Asn Arg Thr Pro
 210 215 220
 Thr Ser Gly Val Thr Pro Asp Met Ala Asp Gln Ile Ala Ser Leu Val
 225 230 235 240
 Leu Ala Lys Leu Gly Lys Asp Ala Thr Lys Pro Gln Gln Val Thr Lys
 245 250 255
 His Thr Ala Lys Glu Val Arg Gln Lys Ile Leu Asn Lys Pro Arg Gln
 260 265 270
 Lys Arg Ser Pro Asn Lys Gln Cys Thr Val Gln Gln Cys Phe Gly Lys

275 280 285
 Arg Gly Pro Asn Gln Asn Phe Gly Gly Gly Glu Met Leu Lys Leu Gly
 290 295 300
 Thr Ser Asp Pro Gln Phe Pro Ile Leu Ala Glu Leu Ala Pro Thr Ala
 305 310 315 320
 Gly Ala Phe Phe Phe Gly Ser Arg Leu Glu Leu Ala Lys Val Gln Asn
 325 330 335
 Leu Ser Gly Asn Pro Asp Glu Pro Gln Lys Asp Val Tyr Glu Leu Arg
 340 345 350
 Tyr Asn Gly Ala Ile Arg Phe Asp Ser Thr Leu Ser Gly Phe Glu Thr
 355 360 365
 Ile Met Lys Val Leu Asn Glu Asn Leu Asn Ala Tyr Gln Gln Gln Asp
 370 375 380
 Gly Met Met Asn Met Ser Pro Lys Pro Gln Arg Gln Arg Gly His Lys
 385 390 395 400
 Asn Gly Gln Gly Glu Asn Asp Asn Ile Ser Val Ala Val Pro Lys Ser
 405 410 415
 Arg Val Gln Gln Asn Lys Ser Arg Glu Leu Thr Ala Glu Asp Ile Ser
 420 425 430
 Leu Leu Lys Lys Met Asp Glu Pro Tyr Thr Glu Asp Thr Ser Glu Ile
 435 440 445
 <210> 50
 <211> 449
 <212> PRT
 <213> porcine hemagglutinating encephalomyelitis
 <400> 50
 Met Ser Phe Thr Pro Gly Lys Gln Ser Ser Ser Arg Ala Ser Ser Gly
 1 5 10 15
 Asn Arg Ser Gly Asn Gly Ile Leu Lys Trp Ala Asp Gln Ser Asp Gln
 20 25 30
 Ser Arg Asn Val Gln Thr Arg Gly Arg Arg Val Gln Ser Lys Gln Thr
 35 40 45

Ala Thr Ser Gln Gln Pro Ser Gly Gly Thr Val Val Pro Tyr Tyr Ser
50 55 60

Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu Phe Glu Phe
65 70 75 80

Ala Glu Gly Gln Gly Val Pro Ile Ala Pro Gly Val Pro Ser Thr Glu
85 90 95

Ala Lys Gly Tyr Trp Tyr Arg His Asn Arg Arg Ser Phe Lys Thr Ala
100 105 110

Asp Gly Asn Gln Arg Gln Leu Leu Pro Arg Trp Tyr Phe Tyr Tyr Leu
115 120 125

Gly Thr Gly Pro His Ala Lys Asp Gln Tyr Gly Thr Asp Ile Asp Gly
130 135 140

Val Phe Trp Val Ala Ser Asn Gln Ala Asp Ile Asn Thr Pro Ala Asp
145 150 155 160

Ile Val Asp Arg Asp Pro Ser Ser Asp Glu Ala Ile Pro Thr Arg Phe
165 170 175

Pro Pro Gly Thr Val Leu Pro Gln Gly Tyr Tyr Ile Glu Gly Ser Gly
180 185 190

Arg Ser Ala Pro Asn Ser Arg Ser Thr Ser Arg Ala Pro Asn Arg Ala
195 200 205

Pro Ser Ala Gly Ser Arg Ser Arg Ala Asn Ser Gly Asn Arg Thr Ser
210 215 220

Thr Pro Gly Val Thr Pro Asp Met Ala Asp Gln Ile Ala Ser Leu Val
225 230 235 240

Leu Ala Lys Leu Gly Lys Asp Ala Thr Lys Pro Gln Gln Val Thr Lys
245 250 255

Gln Thr Ala Lys Glu Val Arg Gln Lys Ile Leu Asn Lys Pro Arg Gln
260 265 270

Lys Arg Ser Pro Asn Lys Gln Cys Thr Val Gln Gln Cys Phe Gly Lys
275 280 285

Arg Gly Pro Asn Gln Asn Phe Gly Gly Gly Glu Met Leu Lys Leu Gly
 290 295 300

Thr Ser Asp Pro Gln Phe Pro Ile Leu Ala Glu Leu Ala Pro Thr Ala
 305 310 315 320

Gly Ala Phe Phe Phe Gly Ser Arg Leu Glu Leu Ala Lys Val Gln Asn
 325 330 335

Leu Ser Gly Asn Pro Asp Glu Pro Gln Lys Asp Val Tyr Glu Leu Arg
 340 345 350

Tyr Asn Gly Ala Ile Arg Phe Asp Ser Thr Leu Ser Gly Phe Glu Thr
 355 360 365

Ile Met Lys Val Leu Asn Gln Asn Leu Asn Ala Tyr Gln His Gln Glu
 370 375 380

Asp Gly Met Met Asn Ile Ser Pro Lys Pro Gln Arg Gln Arg Gly Gln
 385 390 395 400

Lys Asn Gly Gln Val Glu Asn Asp Asn Val Ser Val Ala Ala Pro Lys
 405 410 415

Ser Arg Val Gln Gln Asn Lys Ser Arg Glu Leu Thr Ala Glu Asp Ile
 420 425 430

Ser Leu Leu Lys Lys Met Asp Glu Pro Tyr Thr Glu Asp Thr Ser Glu
 435 440 445

Ile

<210> 51
 <211> 409
 <212> PRT
 <213> turkey coronavirus

<400> 51

Met Ala Ser Gly Lys Ala Thr Gly Lys Thr Asp Ala Pro Ala Pro Ile
 1 5 10 15

Ile Lys Leu Gly Gly Pro Lys Pro Pro Lys Val Gly Ser Ser Gly Asn
 20 25 30

Ala Ser Trp Phe Gln Ser Ile Lys Ala Lys Lys Leu Asn Ser Pro Gln
 35 40 45

Pro Lys Phe Glu Gly Ser Gly Val Pro Asp Asn Glu Asn Ile Lys Thr
 50 55 60
 Ser Gln Gln His Gly Tyr Trp Arg Arg Gln Ala Arg Phe Lys Pro Gly
 65 70 75 80
 Lys Gly Gly Arg Lys Pro Val Pro Asp Ala Trp Tyr Phe Tyr Tyr Thr
 85 90 95
 Gly Thr Gly Pro Ala Ala Asp Leu Asn Trp Gly Asp Thr Gln Asp Gly
 100 105 110
 Ile Val Trp Val Ala Ala Lys Gly Ala Asp Val Lys Ser Arg Ser Asn
 115 120 125
 Gln Gly Thr Arg Asp Pro Asp Lys Phe Asp Gln Tyr Pro Leu Arg Phe
 130 135 140
 Ser Asp Gly Gly Pro Asp Ser Asn Phe Arg Trp Asp Phe Ile Pro Leu
 145 150 155 160
 His Arg Gly Arg Ser Gly Arg Ser Thr Ala Ala Ser Ser Ala Ala Ser
 165 170 175
 Ser Arg Ala Pro Ser Arg Asp Gly Ser Arg Gly Arg Arg Ser Gly Ser
 180 185 190
 Glu Asp Asp Leu Ile Ala Arg Ala Ala Lys Ile Ile Gln Asp Gln Gln
 195 200 205
 Lys Lys Gly Ser Arg Ile Thr Lys Ala Lys Ala Asp Glu Met Ala His
 210 215 220
 Arg Arg Tyr Cys Lys Arg Thr Val Pro Pro Gly Tyr Lys Val Asp Gln
 225 230 235 240
 Val Phe Gly Pro Arg Thr Lys Gly Lys Glu Gly Asn Phe Gly Asp Asp
 245 250 255
 Lys Met Asn Glu Glu Gly Ile Lys Asp Gly Arg Val Thr Ala Met Leu
 260 265 270
 Asn Leu Val Pro Ser Ser His Ala Cys Leu Phe Gly Ser Arg Val Thr
 275 280 285

Pro Lys Leu Gln Pro Asp Gly Leu His Leu Arg Phe Glu Phe Thr Thr
 290 295 300

Val Val Pro Arg Asp Asp Pro Gln Phe Asp Asn Tyr Val Thr Ile Cys
 305 310 315 320

Asp Gln Cys Val Asp Gly Ile Gly Thr Arg Pro Lys Asp Asn Glu Pro
 325 330 335

Arg Pro Lys Ser Arg Pro Ser Ser Arg Pro Ala Thr Arg Gly Asn Ser
 340 345 350

Pro Ala Pro Arg Gln Gln Arg Pro Lys Lys Glu Lys Lys Pro Lys Lys
 355 360 365

Gln Asp Asp Glu Val Asp Lys Ala Leu Thr Ser Asp Glu Glu Arg Asn
 370 375 380

Asn Ala Gln Leu Glu Phe Asp Asp Glu Pro Lys Val Ile Asn Trp Gly
 385 390 395 400

Asp Ser Ala Leu Gly Glu Asn His Leu
 405

<210> 52

<211> 1173

<212> PRT

<213> Human coronavirus 229E

<400> 52

Met Phe Val Leu Leu Val Ala Tyr Ala Leu Leu His Ile Ala Gly Cys
 1 5 10 15

Gln Thr Thr Asn Gly Leu Asn Thr Ser Tyr Ser Val Cys Asn Gly Cys
 20 25 30

Val Gly Tyr Ser Glu Asn Val Phe Ala Val Glu Ser Gly Gly Tyr Ile
 35 40 45

Pro Ser Asp Phe Ala Phe Asn Asn Trp Phe Leu Leu Thr Asn Thr Ser
 50 55 60

Ser Val Val Asp Gly Val Val Arg Ser Phe Gln Pro Leu Leu Leu Asn
 65 70 75 80

Cys Leu Trp Ser Val Ser Gly Leu Arg Phe Thr Thr Gly Phe Val Tyr

	85		90		95
Phe Asn Gly Thr Gly Arg Gly Asp Cys Lys Gly Phe Ser Ser Asp Val	100		105		110
Leu Ser Asp Val Ile Arg Tyr Asn Leu Asn Phe Glu Glu Asn Leu Arg	115		120		125
Arg Gly Thr Ile Leu Phe Lys Thr Ser Tyr Gly Val Val Val Phe Tyr	130		135		140
Cys Thr Asn Asn Thr Leu Val Ser Gly Asp Ala His Ile Pro Phe Gly	145		150		155
Thr Val Leu Gly Asn Phe Tyr Cys Phe Val Asn Thr Thr Ile Gly Thr		165		170	175
Glu Thr Thr Ser Ala Phe Val Gly Ala Leu Pro Lys Thr Val Arg Glu		180		185	190
Phe Val Ile Ser Arg Thr Gly His Phe Tyr Ile Asn Gly Tyr Arg Tyr		195		200	205
Phe Thr Leu Gly Asn Val Glu Ala Val Asn Phe Asn Val Thr Thr Ala		210		215	220
Glu Thr Thr Asp Phe Phe Thr Val Ala Leu Ala Ser Tyr Ala Asp Val		225		230	235
Leu Val Asn Val Ser Gln Thr Ser Ile Ala Asn Ile Ile Tyr Cys Asn		245		250	255
Ser Val Ile Asn Arg Leu Arg Cys Asp Gln Leu Ser Phe Tyr Val Pro		260		265	270
Asp Gly Phe Tyr Ser Thr Ser Pro Ile Gln Ser Val Glu Leu Pro Val		275		280	285
Ser Ile Val Ser Leu Pro Val Tyr His Lys His Met Phe Ile Val Leu		290		295	300
Tyr Val Asp Phe Lys Pro Gln Ser Gly Gly Gly Lys Cys Phe Asn Cys		305		310	315
Tyr Pro Ala Gly Val Asn Ile Thr Leu Ala Asn Phe Asn Glu Thr Lys		325		330	335

Gly Pro Leu Cys Val Asp Thr Ser His Phe Thr Thr Lys Tyr Val Ala
340 345 350

Val Tyr Ala Asn Val Gly Arg Trp Ser Ala Ser Ile Asn Thr Gly Asn
355 360 365

Cys Pro Phe Ser Phe Gly Lys Val Asn Asn Phe Val Lys Phe Gly Ser
370 375 380

Val Cys Phe Ser Leu Lys Asp Ile Pro Gly Gly Cys Ala Met Pro Ile
385 390 395 400

Val Ala Asn Trp Ala Tyr Ser Lys Tyr Tyr Thr Ile Gly Thr Leu Tyr
405 410 415

Val Ser Trp Ser Asp Gly Asp Gly Ile Thr Gly Val Pro Gln Pro Val
420 425 430

Glu Gly Val Ser Ser Phe Met Asn Val Thr Leu Asp Lys Cys Thr Lys
435 440 445

Tyr Asn Ile Tyr Asp Val Ser Gly Val Gly Val Ile Arg Val Ser Asn
450 455 460

Asp Thr Phe Leu Asn Gly Ile Thr Tyr Thr Ser Thr Ser Gly Asn Leu
465 470 475 480

Leu Gly Phe Lys Asp Val Thr Lys Gly Thr Ile Tyr Ser Ile Thr Pro
485 490 495

Cys Asn Pro Pro Asp Gln Leu Val Val Tyr Gln Gln Ala Val Val Gly
500 505 510

Ala Met Leu Ser Glu Asn Phe Thr Ser Tyr Gly Phe Ser Asn Val Val
515 520 525

Glu Leu Pro Lys Phe Phe Tyr Ala Ser Asn Gly Thr Tyr Asn Cys Thr
530 535 540

Asp Ala Val Leu Thr Tyr Ser Ser Phe Gly Val Cys Ala Asp Gly Ser
545 550 555 560

Ile Ile Ala Val Gln Pro Arg Asn Val Ser Tyr Asp Ser Val Ser Ala
565 570 575

Ile Val Thr Ala Asn Leu Ser Ile Pro Ser Asn Trp Thr Ile Ser Val
580 585 590

Gln Val Glu Tyr Leu Gln Ile Thr Ser Thr Pro Ile Val Val Asp Cys
595 600 605

Ser Thr Tyr Val Cys Asn Gly Asn Val Arg Cys Val Glu Leu Leu Lys
610 615 620

Gln Tyr Thr Ser Ala Cys Lys Thr Ile Glu Asp Ala Leu Arg Asn Ser
625 630 635 640

Ala Arg Leu Glu Ser Ala Asp Val Ser Glu Met Leu Thr Phe Asp Lys
645 650 655

Lys Ala Phe Thr Leu Ala Asn Val Ser Ser Phe Gly Asp Tyr Asn Leu
660 665 670

Ser Ser Val Ile Pro Ser Leu Pro Thr Ser Gly Ser Arg Val Ala Gly
675 680 685

Arg Ser Ala Ile Glu Asp Ile Leu Phe Ser Lys Ile Val Thr Ser Gly
690 695 700

Leu Gly Thr Val Asp Ala Asp Tyr Lys Asn Cys Thr Lys Gly Leu Ser
705 710 715 720

Ile Ala Asp Leu Ala Cys Ala Gln Tyr Tyr Asn Gly Ile Met Val Leu
725 730 735

Pro Gly Val Ala Asp Ala Glu Arg Met Ala Met Tyr Thr Gly Ser Leu
740 745 750

Ile Gly Gly Ile Ala Leu Gly Gly Leu Thr Ser Ala Val Ser Ile Pro
755 760 765

Phe Ser Leu Ala Ile Gln Ala Arg Leu Asn Tyr Val Ala Leu Gln Thr
770 775 780

Asp Val Leu Gln Glu Asn Gln Lys Ile Leu Ala Ala Ser Phe Asn Lys
785 790 795 800

Ala Met Thr Asn Ile Val Asp Ala Phe Thr Gly Val Asn Asp Ala Ile
805 810 815

Thr Gln Thr Ser Gln Ala Leu Gln Thr Val Ala Thr Ala Leu Asn Lys
 820 825 830
 Ile Gln Asp Val Val Asn Gln Gln Gly Asn Ser Leu Asn His Leu Thr
 835 840 845
 Ser Gln Leu Arg Gln Asn Phe Gln Ala Ile Ser Ser Ser Ile Gln Ala
 850 855 860
 Ile Tyr Asp Arg Leu Asp Thr Ile Gln Ala Asp Gln Gln Val Asp Arg
 865 870 875 880
 Leu Ile Thr Gly Arg Leu Ala Ala Leu Asn Val Phe Val Ser His Thr
 885 890 895
 Leu Thr Lys Tyr Thr Glu Val Arg Ala Ser Arg Gln Leu Ala Gln Gln
 900 905 910
 Lys Val Asn Glu Cys Val Lys Ser Gln Ser Lys Arg Tyr Gly Phe Cys
 915 920 925
 Gly Asn Gly Thr His Ile Phe Ser Ile Val Asn Ala Ala Pro Glu Gly
 930 935 940
 Leu Val Phe Leu His Thr Val Leu Leu Pro Thr Gln Tyr Lys Asp Val
 945 950 955 960
 Glu Ala Trp Ser Gly Leu Cys Val Asp Gly Thr Asn Gly Tyr Val Leu
 965 970 975
 Arg Gln Pro Asn Leu Ala Leu Tyr Lys Glu Gly Asn Tyr Tyr Arg Ile
 980 985 990
 Thr Ser Arg Ile Met Phe Glu Pro Arg Ile Pro Thr Met Ala Asp Phe
 995 1000 1005
 Val Gln Ile Glu Asn Cys Asn Val Thr Phe Val Asn Ile Ser Arg
 1010 1015 1020
 Ser Glu Leu Gln Thr Ile Val Pro Glu Tyr Ile Asp Val Asn Lys
 1025 1030 1035
 Thr Leu Gln Glu Leu Ser Tyr Lys Leu Pro Asn Tyr Thr Val Pro
 1040 1045 1050
 Asp Leu Val Val Glu Gln Tyr Asn Gln Thr Ile Leu Asn Leu Thr

1055 1060 1065
 Ser Glu Ile Ser Thr Leu Glu Asn Lys Ser Ala Glu Leu Asn Tyr
 1070 1075 1080
 Thr Val Gln Lys Leu Gln Thr Leu Ile Asp Asn Ile Asn Ser Thr
 1085 1090 1095
 Leu Val Asp Leu Lys Trp Leu Asn Arg Val Glu Thr Tyr Ile Lys
 1100 1105 1110
 Trp Pro Trp Trp Val Trp Leu Cys Ile Ser Val Val Leu Ile Phe
 1115 1120 1125
 Val Val Ser Met Leu Leu Leu Cys Cys Cys Ser Thr Gly Cys Cys
 1130 1135 1140
 Gly Phe Phe Ser Cys Phe Ala Ser Ser Ile Arg Gly Cys Cys Glu
 1145 1150 1155
 Ser Thr Lys Leu Pro Tyr Tyr Asp Val Glu Lys Ile His Ile Gln
 1160 1165 1170

 <210> 53
 <211> 1164
 <212> PRT
 <213> Avian infectious bronchitis virus

 <400> 53
 Met Leu Gly Lys Ser Leu Phe Leu Val Thr Ile Leu Cys Ala Leu Cys
 1 5 10 15
 Ser Ala Asn Leu Phe Asp Pro Ala Asn Tyr Val Tyr Tyr Tyr Gln Ser
 20 25 30
 Ala Phe Arg Pro Ser Asn Gly Trp His Leu Gln Gly Gly Ala Tyr Ala
 35 40 45
 Val Val Asn Ser Ser Asn Tyr Ala Asn Asn Ala Gly Ser Ala Ser Glu
 50 55 60
 Cys Thr Val Gly Val Ile Lys Asp Val Tyr Asn Gln Ser Ala Ala Ser
 65 70 75 80
 Ile Ala Met Thr Ala Pro Leu Gln Gly Met Ala Trp Ser Lys Ser Gln
 85 90 95

Phe Cys Ser Ala His Cys Asp Phe Ser Glu Ile Thr Val Phe Val Thr
 100 105 110
 His Cys Tyr Ser Ser Gly Ser Gly Ser Cys Pro Ile Thr Gly Met Ile
 115 120 125
 Ala Arg Gly His Ile Arg Ile Ser Ala Met Lys Asn Gly Ser Leu Phe
 130 135 140
 Tyr Asn Leu Thr Val Ser Val Ser Lys Tyr Pro Asn Phe Lys Ser Phe
 145 150 155 160
 Gln Cys Val Asn Asn Phe Thr Ser Val Tyr Leu Asn Gly Asp Leu Val
 165 170 175
 Phe Thr Ser Asn Lys Thr Thr Asp Val Thr Ser Ala Gly Val Tyr Phe
 180 185 190
 Lys Ala Gly Gly Pro Val Asn Tyr Ser Ile Met Lys Glu Phe Lys Val
 195 200 205
 Leu Ala Tyr Phe Val Asn Gly Thr Ala Gln Asp Val Ile Leu Cys Asp
 210 215 220
 Asn Ser Pro Lys Gly Leu Leu Ala Cys Gln Tyr Asn Thr Gly Asn Phe
 225 230 235 240
 Ser Asp Gly Phe Tyr Pro Phe Thr Asn Ser Thr Leu Val Arg Glu Lys
 245 250 255
 Phe Ile Val Tyr Arg Glu Ser Ser Val Asn Thr Thr Leu Ala Leu Thr
 260 265 270
 Asn Phe Thr Phe Thr Asn Val Ser Asn Ala Gln Pro Asn Ser Gly Gly
 275 280 285
 Val His Thr Phe His Leu Tyr Gln Thr Gln Thr Ala Gln Ser Gly Tyr
 290 295 300
 Tyr Asn Phe Asn Leu Ser Phe Leu Ser Gln Phe Val Tyr Lys Ala Ser
 305 310 315 320
 Asp Tyr Met Tyr Gly Ser Tyr His Pro Ile Cys Ala Phe Arg Pro Glu
 325 330 335

Thr Ile Asn Ser Gly Leu Trp Phe Asn Ser Leu Ser Val Ser Leu Thr
 340 345 350

Tyr Gly Pro Leu Gln Gly Gly Tyr Lys Gln Ser Val Phe Ser Gly Lys
 355 360 365

Ala Thr Cys Cys Tyr Ala Tyr Ser Tyr Asn Gly Pro Arg Ala Cys Lys
 370 375 380

Gly Val Tyr Ser Gly Glu Leu Ser Arg Asp Phe Glu Cys Gly Leu Leu
 385 390 395 400

Val Tyr Val Thr Lys Ser Asp Gly Ser Arg Ile Gln Thr Arg Thr Glu
 405 410 415

Pro Leu Val Leu Thr Gln His Asn Tyr Asn Asn Ile Thr Leu Asp Lys
 420 425 430

Cys Val Ala Tyr Asn Ile Tyr Gly Arg Val Gly Gln Gly Phe Ile Thr
 435 440 445

Asn Val Thr Asp Ser Val Ala Asn Phe Ser Tyr Leu Ala Asp Gly Gly
 450 455 460

Leu Ala Ile Leu Asp Thr Ser Gly Ala Ile Asp Val Phe Val Val Gln
 465 470 475 480

Gly Ser Tyr Gly Leu Asn Tyr Tyr Lys Val Asn Pro Cys Glu Asp Val
 485 490 495

Asn Gln Gln Phe Val Val Ser Gly Gly Asn Ile Val Gly Ile Leu Thr
 500 505 510

Ser Arg Asn Glu Thr Gly Ser Glu Gln Val Glu Asn Gln Phe Tyr Val
 515 520 525

Lys Leu Thr Asn Ser Ser His Arg Arg Arg Arg Ser Ile Gly Gln Asn
 530 535 540

Val Thr Ser Cys Pro Tyr Val Ser Tyr Gly Arg Phe Cys Ile Glu Pro
 545 550 555 560

Asp Gly Ser Leu Lys Met Ile Val Pro Glu Glu Leu Lys Gln Phe Val
 565 570 575

Ala Pro Leu Leu Asn Ile Thr Glu Ser Val Leu Ile Pro Asn Ser Phe

580 585 590
 Asn Leu Thr Val Thr Asp Glu Tyr Ile Gln Thr Arg Met Asp Lys Val
 595 600 605
 Gln Ile Asn Cys Leu Gln Tyr Val Cys Gly Asn Ser Leu Glu Cys Arg
 610 615 620
 Lys Leu Phe Gln Gln Tyr Gly Pro Val Cys Asp Asn Ile Leu Ser Val
 625 630 635 640
 Val Asn Ser Val Ser Gln Lys Glu Asp Met Glu Leu Leu Ser Phe Tyr
 645 650 655
 Ser Ser Thr Lys Pro Lys Gly Tyr Asp Thr Pro Val Leu Ser Asn Val
 660 665 670
 Ser Thr Gly Glu Phe Asn Ile Ser Leu Leu Leu Thr Pro Pro Ser Ser
 675 680 685
 Pro Ser Gly Arg Ser Phe Val Glu Asp Leu Leu Phe Thr Ser Val Glu
 690 695 700
 Thr Val Gly Leu Pro Thr Asp Ala Glu Tyr Lys Lys Cys Thr Ala Gly
 705 710 715 720
 Pro Leu Gly Thr Leu Lys Asp Leu Ile Cys Ala Arg Glu Tyr Asn Gly
 725 730 735
 Leu Leu Val Leu Pro Pro Ile Ile Thr Ala Asp Met Gln Thr Met Tyr
 740 745 750
 Thr Ala Ser Leu Val Gly Ala Met Ala Phe Gly Gly Ile Thr Ser Ala
 755 760 765
 Ala Ala Ile Pro Phe Ala Thr Gln Ile Gln Ala Arg Ile Asn His Leu
 770 775 780
 Gly Ile Ala Gln Ser Leu Leu Met Lys Asn Gln Glu Lys Ile Ala Ala
 785 790 795 800
 Ser Phe Asn Lys Ala Ile Gly His Met Gln Glu Gly Phe Arg Ser Thr
 805 810 815
 Ser Leu Ala Leu Gln Gln Val Gln Asp Val Val Asn Lys Gln Ser Ala
 820 825 830

Ile Leu Thr Glu Thr Met Asn Ser Leu Asn Lys Asn Phe Gly Ala Ile
835 840 845

Ser Ser Val Ile Gln Asp Ile Tyr Ala Gln Leu Asp Ala Ile Gln Ala
850 855 860

Asp Ala Gln Val Asp Arg Leu Ile Thr Gly Arg Leu Ser Ser Leu Ser
865 870 875 880

Val Leu Ala Ser Ala Lys Gln Ser Glu Tyr Ile Arg Val Ser Gln Gln
885 890 895

Arg Glu Leu Ala Thr Gln Lys Ile Asn Glu Cys Val Lys Ser Gln Ser
900 905 910

Asn Arg Tyr Gly Phe Cys Gly Ser Gly Arg His Val Leu Ser Ile Pro
915 920 925

Gln Asn Ala Pro Asn Gly Ile Val Phe Ile His Phe Thr Tyr Thr Pro
930 935 940

Glu Thr Phe Val Asn Val Thr Ala Ile Val Gly Phe Cys Val Asn Pro
945 950 955 960

Leu Asn Ala Ser Gln Tyr Ala Ile Val Pro Ala Asn Gly Arg Gly Ile
965 970 975

Phe Ile Gln Val Asn Gly Thr Tyr Tyr Ile Thr Ser Arg Asp Met Tyr
980 985 990

Met Pro Arg Asp Ile Thr Ala Gly Asp Ile Val Thr Leu Thr Ser Cys
995 1000 1005

Gln Ala Asn Tyr Val Asn Val Asn Lys Thr Val Ile Thr Thr Phe
1010 1015 1020

Val Glu Asp Asp Asp Phe Asn Phe Asp Asp Glu Leu Ser Lys Trp
1025 1030 1035

Trp Asn Asp Thr Lys His Gly Leu Pro Asp Phe Asp Asp Phe Asn
1040 1045 1050

Tyr Thr Val Pro Ile Leu Asn Ile Ser Gly Glu Ile Asp Asn Ile
1055 1060 1065

Gln Gly Val Ile Gln Gly Leu Asn Asp Ser Leu Ile Asn Leu Glu
 1070 1075 1080

Glu Leu Ser Ile Ile Lys Thr Tyr Ile Lys Trp Pro Trp Tyr Val
 1085 1090 1095

Trp Leu Ala Ile Gly Phe Ala Ile Ile Ile Phe Ile Leu Ile Leu
 1100 1105 1110

Gly Trp Val Phe Phe Met Thr Gly Cys Cys Gly Cys Cys Cys Gly
 1115 1120 1125

Cys Phe Gly Ile Ile Pro Leu Ile Ser Lys Cys Gly Lys Lys Ser
 1130 1135 1140

Ser Tyr Tyr Thr Thr Phe Asp Asn Asp Val Val Thr Glu Gln Tyr
 1145 1150 1155

Arg Pro Lys Lys Ser Val
 1160

<210> 54
 <211> 1363
 <212> PRT
 <213> Bovine coronavirus

<400> 54

Met Phe Leu Ile Leu Leu Ile Ser Leu Pro Met Ala Phe Ala Val Ile
 1 5 10 15

Gly Asp Leu Lys Cys Thr Thr Val Ser Ile Asn Asp Val Asp Thr Gly
 20 25 30

Ala Pro Ser Ile Ser Thr Asp Ile Val Asp Val Thr Asn Gly Leu Gly
 35 40 45

Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr Leu Leu Leu
 50 55 60

Asn Gly Tyr Tyr Pro Thr Ser Gly Ser Thr Tyr Arg Asn Met Ala Leu
 65 70 75 80

Lys Gly Thr Leu Leu Leu Ser Arg Leu Trp Phe Lys Pro Pro Phe Leu
 85 90 95

Ser Asp Phe Ile Asn Gly Ile Phe Ala Lys Val Lys Asn Thr Lys Val

100 105 110
 Ile Lys Lys Gly Val Met Tyr Ser Glu Phe Pro Ala Ile Thr Ile Gly
 115 120 125
 Ser Thr Phe Val Asn Thr Ser Tyr Ser Val Val Val Gln Pro His Thr
 130 135 140
 Thr Asn Leu Asp Asn Lys Leu Gln Gly Leu Leu Glu Ile Ser Val Cys
 145 150 155 160
 Gln Tyr Thr Met Cys Glu Tyr Pro His Thr Ile Cys His Pro Lys Leu
 165 170 175
 Gly Asn Lys Arg Val Glu Leu Trp His Trp Asp Thr Gly Val Val Ser
 180 185 190
 Cys Leu Tyr Lys Arg Asn Phe Thr Tyr Asp Val Asn Ala Asp Tyr Leu
 195 200 205
 Tyr Phe His Phe Tyr Gln Glu Gly Gly Thr Phe Tyr Ala Tyr Phe Thr
 210 215 220
 Asp Thr Gly Val Val Thr Lys Phe Leu Phe Asn Val Tyr Leu Gly Thr
 225 230 235 240
 Val Leu Ser His Tyr Tyr Val Leu Pro Leu Thr Cys Ser Ser Ala Met
 245 250 255
 Thr Leu Glu Tyr Trp Val Thr Pro Leu Thr Ser Lys Gln Tyr Leu Leu
 260 265 270
 Ala Phe Asn Gln Asp Gly Val Ile Phe Asn Ala Val Asp Cys Lys Ser
 275 280 285
 Asp Phe Met Ser Glu Ile Lys Cys Lys Thr Leu Ser Ile Ala Pro Ser
 290 295 300
 Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Ile Ala Asp
 305 310 315 320
 Val Tyr Arg Arg Ile Pro Asn Leu Pro Asp Cys Asn Ile Glu Ala Trp
 325 330 335
 Leu Asn Asp Lys Ser Val Pro Ser Pro Leu Asn Trp Glu Arg Lys Thr
 340 345 350

Phe Ser Asn Cys Asn Phe Asn Met Ser Ser Leu Met Ser Phe Ile Gln
 355 360 365

Ala Asp Ser Phe Thr Cys Asn Asn Ile Asp Ala Ala Lys Ile Tyr Gly
 370 375 380

Met Cys Phe Ser Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Gly
 385 390 395 400

Arg Lys Val Asp Leu Gln Leu Gly Asn Leu Gly Tyr Leu Gln Ser Phe
 405 410 415

Asn Tyr Arg Ile Asp Thr Thr Ala Thr Ser Cys Gln Leu Tyr Tyr Asn
 420 425 430

Leu Pro Ala Ala Asn Val Ser Val Ser Arg Phe Asn Pro Ser Thr Trp
 435 440 445

Asn Arg Arg Phe Gly Phe Thr Glu Gln Phe Val Phe Lys Pro Gln Pro
 450 455 460

Val Gly Val Phe Thr His His Asp Val Val Tyr Ala Gln His Cys Phe
 465 470 475 480

Lys Ala Pro Lys Asn Phe Cys Pro Cys Lys Leu Asp Gly Ser Leu Cys
 485 490 495

Val Gly Asn Gly Pro Gly Ile Asp Ala Gly Tyr Lys Asn Ser Gly Ile
 500 505 510

Gly Thr Cys Pro Ala Gly Thr Asn Tyr Leu Thr Cys His Asn Ala Ala
 515 520 525

Gln Cys Asp Cys Leu Cys Thr Pro Asp Pro Ile Thr Ser Lys Ser Thr
 530 535 540

Gly Pro Tyr Lys Cys Pro Gln Thr Lys Tyr Leu Val Gly Ile Gly Glu
 545 550 555 560

His Cys Ser Gly Leu Ala Ile Lys Ser Asp Tyr Cys Gly Gly Asn Pro
 565 570 575

Cys Thr Cys Gln Pro Gln Ala Phe Leu Gly Trp Ser Val Asp Ser Cys
 580 585 590

Leu Gln Gly Asp Arg Cys Asn Ile Phe Ala Asn Phe Ile Phe His Asp
595 600 605

Val Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln Lys Ser Asn Thr
610 615 620

Asp Ile Ile Leu Gly Val Cys Val Asn Tyr Asp Leu Tyr Gly Ile Thr
625 630 635 640

Gly Gln Gly Ile Phe Val Glu Val Asn Ala Thr Tyr Tyr Asn Ser Trp
645 650 655

Gln Asn Leu Leu Tyr Asp Ser Asn Gly Asn Leu Tyr Gly Phe Arg Asp
660 665 670

Tyr Leu Thr Asn Arg Thr Phe Met Ile Arg Ser Cys Tyr Ser Gly Arg
675 680 685

Val Ser Ala Ala Phe His Ala Asn Ser Ser Glu Pro Ala Leu Leu Phe
690 695 700

Arg Asn Ile Lys Cys Asn Tyr Val Phe Asn Asn Thr Leu Ser Arg Gln
705 710 715 720

Leu Gln Pro Ile Asn Tyr Phe Asp Ser Tyr Leu Gly Cys Val Val Asn
725 730 735

Ala Asp Asn Ser Thr Ser Ser Val Val Gln Thr Cys Asp Leu Thr Val
740 745 750

Gly Ser Gly Tyr Cys Val Asp Tyr Ser Thr Lys Arg Arg Ser Arg Arg
755 760 765

Ala Ile Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe Thr Val
770 775 780

Asn Ser Val Asn Asp Ser Leu Glu Pro Val Gly Gly Leu Tyr Glu Ile
785 790 795 800

Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Met Glu Glu Phe Ile Gln
805 810 815

Thr Ser Ser Pro Lys Val Thr Ile Asp Cys Ser Ala Phe Val Cys Gly
820 825 830

Asp Tyr Ala Ala Cys Lys Ser Gln Leu Val Glu Tyr Gly Ser Phe Cys
835 840 845

Asp Asn Ile Asn Ala Ile Leu Thr Glu Val Asn Glu Leu Leu Asp Thr
850 855 860

Thr Gln Leu Gln Val Ala Asn Ser Leu Met Asn Gly Val Thr Leu Ser
865 870 875 880

Thr Lys Leu Lys Asp Gly Val Asn Phe Asn Val Asp Asp Ile Asn Phe
885 890 895

Ser Pro Val Leu Gly Cys Leu Gly Ser Ala Cys Asn Lys Val Ser Ser
900 905 910

Arg Ser Ala Ile Glu Asp Leu Leu Phe Ser Lys Val Lys Leu Ser Asp
915 920 925

Val Gly Phe Val Glu Ala Tyr Asn Asn Cys Thr Gly Gly Ala Glu Ile
930 935 940

Arg Asp Leu Ile Cys Val Gln Ser Tyr Asn Gly Ile Lys Val Leu Pro
945 950 955 960

Pro Leu Leu Ser Val Asn Gln Ile Ser Gly Tyr Thr Leu Ala Ala Thr
965 970 975

Ser Ala Ser Leu Phe Pro Pro Leu Ser Ala Ala Val Gly Val Pro Phe
980 985 990

Tyr Leu Asn Val Gln Tyr Arg Ile Asn Gly Ile Gly Val Thr Met Asp
995 1000 1005

Val Leu Ser Gln Asn Gln Lys Leu Ile Ala Asn Ala Phe Asn Asn
1010 1015 1020

Ala Leu Asp Ala Ile Gln Glu Gly Phe Asp Ala Thr Asn Ser Ala
1025 1030 1035

Leu Val Lys Ile Gln Ala Val Val Asn Ala Asn Ala Glu Ala Leu
1040 1045 1050

Asn Asn Leu Leu Gln Gln Leu Ser Asn Arg Phe Gly Ala Ile Ser
1055 1060 1065

Ser Ser Leu Gln Glu Ile Leu Ser Arg Leu Asp Ala Leu Glu Ala

1070		1075		1080
Gln Ala 1085	Gln Ile Asp Arg	Leu 1090	Ile Asn Gly Arg	Leu Thr Ala Leu 1095
Asn Val 1100	Tyr Val Ser Gln	Gln 1105	Leu Ser Asp Ser	Thr Leu Val Lys 1110
Phe Ser 1115	Ala Ala Gln Ala	Met 1120	Glu Lys Val Asn	Glu Cys Val Lys 1125
Ser Gln 1130	Ser Ser Arg Ile	Asn 1135	Phe Cys Gly Asn	Gly Asn His Ile 1140
Ile Ser 1145	Leu Val Gln Asn	Ala 1150	Pro Tyr Gly Leu	Tyr Phe Ile His 1155
Phe Ser 1160	Tyr Val Pro Thr	Lys 1165	Tyr Val Thr Ala	Lys Val Ser Pro 1170
Gly Leu 1175	Cys Ile Ala Gly	Asp 1180	Arg Gly Ile Ala	Pro Lys Ser Gly 1185
Tyr Phe 1190	Val Asn Val Asn	Asn 1195	Thr Trp Met Phe	Thr Gly Ser Gly 1200
Tyr Tyr 1205	Tyr Pro Glu Pro	Ile 1210	Thr Gly Asn Asn	Val Val Val Met 1215
Ser Thr 1220	Cys Ala Val Asn	Tyr 1225	Thr Lys Ala Pro	Asp Val Met Leu 1230
Asn Ile 1235	Ser Thr Pro Asn	Leu 1240	His Asp Phe Lys	Glu Glu Leu Asp 1245
Gln Trp 1250	Phe Lys Asn Gln	Thr 1255	Ser Val Ala Pro	Asp Leu Ser Leu 1260
Asp Tyr 1265	Ile Asn Val Thr	Phe 1270	Leu Asp Leu Gln	Asp Glu Met Asn 1275
Arg Leu 1280	Gln Glu Ala Ile	Lys 1285	Val Leu Asn Gln	Ser Tyr Ile Asn 1290
Leu Lys 1295	Asp Ile Gly Thr	Tyr 1300	Glu Tyr Tyr Val	Lys Trp Pro Trp 1305

Tyr Val Trp Leu Leu Ile Gly Phe Ala Gly Val Ala Met Leu Val
 1310 1315 1320

Leu Leu Phe Phe Ile Cys Cys Cys Thr Gly Cys Gly Thr Ser Cys
 1325 1330 1335

Phe Lys Ile Cys Gly Gly Cys Cys Asp Asp Tyr Thr Gly His Gln
 1340 1345 1350

Glu Leu Val Ile Lys Thr Ser His Asp Asp
 1355 1360

<210> 55
 <211> 1453
 <212> PRT
 <213> canine coronavirus

<400> 55

Met Ile Val Leu Ile Leu Cys Leu Leu Leu Phe Ser Tyr Asn Ser Val
 1 5 10 15

Ile Cys Thr Ser Asn Asn Asp Cys Val Gln Gly Asn Val Thr Gln Leu
 20 25 30

Pro Gly Asn Glu Asn Ile Ile Lys Asp Phe Leu Phe His Thr Phe Lys
 35 40 45

Glu Glu Pro Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val Trp
 50 55 60

Tyr Asn Cys Ser Arg Ser Ala Thr Thr Thr Ala Tyr Lys Asp Phe Ser
 65 70 75 80

Asn Ile His Ala Phe Tyr Phe Asp Met Glu Ala Met Glu Asn Ser Thr
 85 90 95

Gly Asn Ala Arg Gly Lys Pro Leu Leu Val His Val His Gly Asp Pro
 100 105 110

Val Ser Ile Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Pro
 115 120 125

Arg Pro Leu Leu Lys His Gly Leu Leu Cys Ile Thr Lys Asn Lys Ile
 130 135 140

Ile Asp Tyr Asn Thr Phe Thr Ser Ala Gln Trp Ser Ala Ile Cys Leu
 145 150 155 160

Gly Asp Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly
 165 170 175

Thr Lys Ile Phe Gly Leu Glu Trp Asn Asp Asp Tyr Val Thr Ala Tyr
 180 185 190

Ile Ser Asp Arg Ser His His Leu Asn Ile Asn Asn Asn Trp Phe Asn
 195 200 205

Asn Val Thr Ile Leu Tyr Ser Arg Ser Ser Ser Ala Thr Trp Gln Lys
 210 215 220

Ser Ala Ala Tyr Val Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr Lys
 225 230 235 240

Leu Asn Asn Thr Asn Gly Leu Lys Ser Tyr Glu Leu Cys Glu Asp Tyr
 245 250 255

Glu Tyr Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Val Gly
 260 265 270

Gly Tyr Ile Pro His Gly Phe Ser Phe Asn Asn Trp Phe Met Arg Thr
 275 280 285

Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro Leu
 290 295 300

Leu Val Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala Gln
 305 310 315 320

Gln Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val Ser
 325 330 335

Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr Ala
 340 345 350

Leu Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr Thr
 355 360 365

Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Asn Asp Thr Val Ser Glu
 370 375 380

Ser Ser Phe Tyr Ser Tyr Gly Glu Ile Ser Phe Gly Val Thr Asp Gly

105

Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val Val
645 650 655

Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly Val
660 665 670

Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu Asp
675 680 685

Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Ile Thr Gly Val Gly Ile Ile
690 695 700

Arg Gln Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser Leu
705 710 715 720

Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile Tyr
725 730 735

Ser Val Thr Pro Cys Asp Val Ser Ala His Ala Ala Val Ile Asp Gly
740 745 750

Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly Leu
755 760 765

Thr His Trp Thr Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr Asn
770 775 780

Tyr Thr Asn Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp Val
785 790 795 800

Asp Cys Glu Pro Ile Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys Asn
805 810 815

Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val Gln
820 825 830

Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile Ser
835 840 845

Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile Asp
850 855 860

Cys Ser Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu Leu
865 870 875 880

Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala Met
885 890 895

Gly Ala Arg Leu Glu Asn Met Glu Ile Asp Ser Met Leu Phe Val Ser
900 905 910

Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr Glu
915 920 925

Thr Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser Trp
930 935 940

Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg Lys
945 950 955 960

Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr Ser
965 970 975

Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly Tyr
980 985 990

Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met Val
995 1000 1005

Leu Pro Gly Val Ala Asn Asp Asp Lys Met Ala Met Tyr Thr Ala
1010 1015 1020

Ser Leu Ala Gly Gly Ile Thr Leu Gly Ser Leu Gly Gly Gly Ala
1025 1030 1035

Val Ser Ile Pro Phe Ala Ile Ala Val Gln Ala Arg Leu Asn Tyr
1040 1045 1050

Val Ala Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu
1055 1060 1065

Ala Asn Ala Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe
1070 1075 1080

Gly Lys Val Asn Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala
1085 1090 1095

Thr Val Ala Lys Val Leu Ala Lys Val Gln Asp Val Val Asn Thr
1100 1105 1110

Gln Gly 1115	Gln Ala Leu Ser 1120	His 1125	Leu Thr Leu Gln 1130	Leu 1135	Gln Asn Asn 1140								
Phe Gln 1130	Ala Ile Ser Ser 1135	Ser 1140	Ile Ser Asp Ile 1145	Tyr 1150	Asn Arg Leu 1155								
Asp Glu 1145	Leu Ser Ala Asp 1150	Ala 1155	Gln Val Asp Arg 1160	Leu 1165	Ile Thr Gly 1170								
Arg Leu 1160	Thr Ala Leu Asn 1165	Ala 1170	Phe Val Ser Gln 1175	Thr 1180	Leu Thr Arg 1185								
Gln Ala 1175	Glu Val Arg Ala 1180	Ser 1185	Arg Gln Leu Ala 1190	Lys 1195	Asp Lys Val 1200								
Asn Glu 1190	Cys Val Arg Ser 1195	Gln 1200	Ser Gln Arg Phe 1205	Gly 1210	Phe Cys Gly 1215								
Asn Gly 1205	Thr His Leu Phe 1210	Ser 1215	Leu Ala Asn Ala 1220	Ala 1225	Pro Asn Gly 1230								
Met Ile 1220	Phe Phe His Thr 1225	Val 1230	Leu Leu Pro Thr 1235	Ala 1240	Tyr Glu Thr 1245								
Val Thr 1235	Ala Trp Ser Gly 1240	Ile 1245	Cys Ala Ser Asp 1250	Gly 1255	Asp Arg Thr 1260								
Phe Gly 1250	Leu Val Val Lys 1255	Asp 1260	Val Gln Leu Thr 1265	Leu 1270	Phe Arg Asn 1275								
Leu Asp 1265	Asp Lys Phe Tyr 1270	Leu 1275	Thr Pro Arg Thr 1280	Met 1285	Tyr Gln Pro 1290								
Ile Val 1280	Ala Thr Ser Ser 1285	Asp 1290	Phe Val Gln Ile 1295	Glu 1300	Gly Cys Asp 1305								
Val Leu 1295	Phe Val Asn Ala 1300	Thr 1305	Val Ile Asp Leu 1310	Pro 1315	Ser Ile Ile 1320								
Pro Asp 1310	Tyr Ile Asp Ile 1315	Asn 1320	Gln Thr Val Gln 1325	Asp 1330	Ile Leu Glu 1335								
Asn Phe 1325	Arg Pro Asn Trp 1330	Thr 1335	Val Pro Glu Leu 1340	Pro 1345	Leu Asp Ile 1350								
Phe Asn 1340	Ala Thr Tyr Leu 1345	Asn 1350	Leu Thr Gly Glu 1355	Ile 1360	Asn Asp Leu 1365								

1340 1345 1350
 Glu Phe Arg Ser Glu Lys Leu His Asn Thr Thr Val Glu Leu Ala
 1355 1360 1365
 Ile Leu Ile Asp Asn Ile Asn Asn Thr Leu Val Asn Leu Glu Trp
 1370 1375 1380
 Leu Asn Arg Ile Glu Thr Tyr Val Lys Trp Pro Trp Tyr Val Trp
 1385 1390 1395
 Leu Leu Ile Gly Leu Val Val Ile Phe Cys Ile Pro Ile Leu Leu
 1400 1405 1410
 Phe Cys Cys Cys Ser Thr Gly Cys Cys Gly Cys Ile Gly Cys Leu
 1415 1420 1425
 Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg Gln Phe Glu Ser
 1430 1435 1440
 Tyr Glu Pro Ile Glu Lys Val His Val His
 1445 1450

 <210> 56
 <211> 1464
 <212> PRT
 <213> Feline infectious peritonitis virus

 <400> 56

 Met Ile Phe Ile Ile Leu Thr Leu Leu Ser Val Ala Lys Ser Glu Asp
 1 5 10 15

 Ala Pro His Gly Val Thr Leu Pro Gln Phe Asn Thr Ser His Asn Asn
 20 25 30

 Glu Arg Phe Glu Leu Asn Phe Tyr Asn Phe Leu Gln Thr Trp Asp Ile
 35 40 45

 Pro Pro Asn Thr Glu Thr Ile Leu Gly Gly Tyr Leu Pro Tyr Cys Gly
 50 55 60

 Ala Gly Val Asn Cys Gly Trp Tyr Asn Phe Ser Gln Ser Val Gly Gln
 65 70 75 80

 Asn Gly Lys Tyr Ala Tyr Ile Asn Thr Gln Asn Leu Asn Ile Pro Asn
 85 90 95

Val His Gly Val Tyr Phe Asp Val Arg Glu His Asn Asn Asp Gly Glu
 100 105 110
 Trp Asp Asp Arg Asp Lys Val Gly Leu Leu Ile Ala Ile His Gly Asn
 115 120 125
 Ser Lys Tyr Ser Leu Leu Met Val Leu Gln Asp Ala Val Glu Ala Asn
 130 135 140
 Gln Pro His Val Ala Val Lys Ile Cys His Trp Lys Pro Gly Asn Ile
 145 150 155 160
 Ser Ser Tyr His Ala Phe Ser Val Asn Leu Gly Asp Gly Gly Gln Cys
 165 170 175
 Val Phe Asn Gln Arg Phe Ser Leu Asp Thr Val Leu Thr Thr Asn Asp
 180 185 190
 Phe Tyr Gly Phe Gln Trp Thr Asp Thr Tyr Val Asp Ile Tyr Leu Gly
 195 200 205
 Gly Thr Ile Thr Lys Val Trp Val Asp Asn Asp Trp Ser Ile Val Glu
 210 215 220
 Ala Ser Ile Ser Tyr His Trp Asn Arg Ile Asn Tyr Gly Tyr Tyr Met
 225 230 235 240
 Gln Phe Val Asn Arg Thr Thr Tyr Tyr Ala Tyr Asn Asn Thr Gly Gly
 245 250 255
 Ala Asn Tyr Thr Gln Leu Gln Leu Ser Glu Cys His Thr Asp Tyr Cys
 260 265 270
 Ala Gly Tyr Ala Lys Asn Val Phe Val Pro Ile Asp Gly Lys Ile Pro
 275 280 285
 Glu Asp Phe Ser Phe Ser Asn Trp Phe Leu Leu Ser Asp Lys Ser Thr
 290 295 300
 Leu Val Gln Gly Arg Val Leu Ser Ser Gln Pro Val Phe Val Gln Cys
 305 310 315 320
 Leu Arg Pro Val Pro Ser Trp Ser Asn Asn Thr Ala Val Val His Phe
 325 330 335

Lys Asn Asp Ala Phe Cys Pro Asn Val Thr Ala Asp Val Leu Arg Phe
340 345 350

Asn Leu Asn Phe Ser Asp Thr Asp Val Tyr Thr Asp Ser Thr Asn Asp
355 360 365

Glu Gln Leu Phe Phe Thr Phe Glu Asp Asn Thr Thr Ala Ser Ile Ala
370 375 380

Cys Tyr Ser Ser Ala Asn Val Thr Asp Phe Gln Pro Ala Asn Asn Ser
385 390 395 400

Val Ser His Ile Pro Phe Gly Lys Thr Ala His Phe Cys Phe Ala Asn
405 410 415

Phe Ser His Ser Ile Val Ser Arg Gln Phe Leu Gly Ile Leu Pro Pro
420 425 430

Thr Val Arg Glu Phe Ala Phe Gly Arg Asp Gly Ser Ile Phe Val Asn
435 440 445

Gly Tyr Lys Tyr Phe Ser Leu Pro Ala Ile Arg Ser Val Asn Phe Ser
450 455 460

Ile Ser Ser Val Glu Glu Tyr Gly Phe Trp Thr Ile Ala Tyr Thr Asn
465 470 475 480

Tyr Thr Asp Val Met Val Asp Val Asn Gly Thr Ala Ile Thr Arg Leu
485 490 495

Phe Tyr Cys Asp Ser Pro Leu Asn Arg Ile Lys Cys Gln Gln Leu Lys
500 505 510

His Glu Leu Pro Asp Gly Phe Tyr Ser Ala Ser Met Leu Val Lys Lys
515 520 525

Asp Leu Pro Lys Thr Phe Val Thr Met Pro Gln Phe Tyr His Trp Met
530 535 540

Asn Val Thr Leu His Val Val Leu Asn Asp Thr Glu Lys Lys Tyr Asp
545 550 555 560

Ile Ile Leu Ala Lys Ala Pro Glu Leu Ala Ala Leu Ala Asp Val His
565 570 575

Phe Glu Ile Ala Gln Ala Asn Gly Ser Val Thr Asn Val Thr Ser Leu

580	585	590
Cys Val Gln Ala Arg Gln Leu Ala Leu Phe Tyr Lys Tyr Thr Ser Leu 595 600 605		
Gln Gly Leu Tyr Thr Tyr Ser Asn Leu Val Glu Leu Gln Asn Tyr Asp 610 615 620		
Cys Pro Phe Ser Pro Gln Gln Phe Asn Asn Tyr Leu Gln Phe Glu Thr 625 630 635 640		
Leu Cys Phe Asp Val Asn Pro Ala Val Ala Gly Cys Lys Trp Ser Leu 645 650 655		
Val His Asp Val Gln Trp Arg Thr Gln Phe Ala Thr Ile Thr Val Ser 660 665 670		
Tyr Lys His Gly Ser Met Ile Thr Thr His Ala Lys Gly His Ser Trp 675 680 685		
Gly Phe Gln Asp Thr Ser Val Leu Val Lys Asp Glu Cys Thr Asp Tyr 690 695 700		
Asn Ile Tyr Gly Phe Gln Gly Thr Gly Ile Ile Arg Asn Thr Thr Ser 705 710 715 720		
Arg Leu Val Ala Gly Leu Tyr Tyr Thr Ser Ile Ser Gly Asp Leu Leu 725 730 735		
Ala Phe Lys Asn Ser Thr Thr Gly Glu Ile Phe Thr Val Val Pro Cys 740 745 750		
Asp Leu Thr Ala Gln Val Ala Val Ile Asn Asp Glu Ile Val Gly Ala 755 760 765		
Ile Thr Ala Val Asn Gln Thr Asp Leu Phe Glu Phe Val Asn Asn Thr 770 775 780		
Gln Ala Arg Arg Ser Arg Ser Ser Thr Pro Asn Phe Val Thr Ser Tyr 785 790 795 800		
Thr Met Pro Gln Phe Tyr Tyr Ile Thr Lys Trp Asn Asn Asp Thr Ser 805 810 815		
Ser Asn Cys Thr Ser Ala Ile Thr Tyr Ser Ser Phe Ala Ile Cys Asn 820 825 830		

Thr Gly Glu Ile Lys Tyr Val Asn Val Thr His Val Glu Ile Val Asp
835 840 845

Asp Ser Ile Gly Val Ile Lys Pro Val Ser Thr Gly Asn Ile Ser Ile
850 855 860

Pro Lys Asn Phe Thr Val Ala Val Gln Ala Glu Tyr Ile Gln Ile Gln
865 870 875 880

Val Lys Pro Val Val Val Asp Cys Ala Thr Tyr Val Cys Asn Gly Asn
885 890 895

Thr His Cys Leu Lys Leu Leu Thr Gln Tyr Thr Ser Ala Cys Gln Thr
900 905 910

Ile Glu Asn Ala Leu Asn Leu Gly Ala Arg Leu Glu Ser Leu Met Leu
915 920 925

Asn Asp Met Ile Thr Val Ser Asp Arg Gly Leu Glu Leu Ala Thr Val
930 935 940

Glu Arg Phe Asn Ala Thr Ala Leu Gly Gly Glu Lys Leu Gly Gly Leu
945 950 955 960

Tyr Phe Asp Gly Leu Ser Ser Leu Leu Pro Pro Lys Ile Gly Lys Arg
965 970 975

Ser Ala Val Glu Asp Leu Leu Phe Asn Lys Val Val Thr Ser Gly Leu
980 985 990

Gly Thr Val Asp Asp Asp Tyr Lys Lys Cys Ser Ser Gly Thr Asp Val
995 1000 1005

Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met Val Leu
1010 1015 1020

Pro Gly Val Val Asp Gly Asn Lys Met Ser Met Tyr Thr Ala Ser
1025 1030 1035

Leu Ile Gly Gly Met Ala Leu Gly Ser Ile Thr Ser Ala Val Ala
1040 1045 1050

Val Pro Phe Ala Met Gln Val Gln Ala Arg Leu Asn Tyr Val Ala
1055 1060 1065

Leu Gln Thr Asp Val Leu Gln Glu Asn Gln Lys Ile Leu Ala Asn 1070 1075 1080
Ala Phe Asn Asn Ala Ile Gly Asn Ile Thr Leu Ala Leu Gly Lys 1085 1090 1095
Val Ser Asn Ala Ile Thr Thr Thr Ser Asp Gly Phe Asn Ser Met 1100 1105 1110
Ala Ser Ala Leu Thr Lys Ile Gln Ser Val Val Asn Gln Gln Gly 1115 1120 1125
Glu Ala Leu Ser Gln Leu Thr Ser Gln Leu Gln Lys Asn Phe Gln 1130 1135 1140
Ala Ile Ser Ser Ser Ile Ala Glu Ile Tyr Asn Arg Leu Glu Lys 1145 1150 1155
Val Glu Ala Asp Ala Gln Val Asp Arg Leu Ile Thr Gly Arg Leu 1160 1165 1170
Ala Ala Leu Asn Ala Tyr Val Ser Gln Thr Leu Thr Gln Tyr Ala 1175 1180 1185
Glu Val Lys Ala Ser Arg Gln Ile Ala Leu Glu Lys Val Asn Glu 1190 1195 1200
Cys Val Lys Ser Gln Ser Asn Arg Tyr Gly Phe Cys Gly Asn Gly 1205 1210 1215
Thr His Leu Phe Ser Leu Val Asn Ser Ala Pro Glu Gly Leu Leu 1220 1225 1230
Phe Phe His Thr Val Leu Leu Pro Thr Glu Trp Glu Glu Val Thr 1235 1240 1245
Ala Trp Ser Gly Ile Cys Val Asn Asp Thr Tyr Ala Tyr Val Leu 1250 1255 1260
Lys Asp Phe Asp His Ser Ile Phe Ser Tyr Asn Gly Thr Tyr Met 1265 1270 1275
Val Thr Pro Arg Asn Met Phe Gln Pro Arg Lys Pro Gln Met Ser 1280 1285 1290

Asp Phe Val Gln Ile Thr Ser Cys Glu Val Thr Phe Leu Asn Met
 1295 1300 1305
 Thr Tyr Thr Thr Phe Gln Glu Ile Val Ile Asp Tyr Ile Asp Ile
 1310 1315 1320
 Asn Lys Thr Ile Ala Asp Met Leu Glu Gln Tyr Asn Pro Asn Tyr
 1325 1330 1335
 Thr Thr Pro Glu Leu Asn Leu Leu Leu Asp Ile Phe Asn Gln Thr
 1340 1345 1350
 Lys Leu Asn Leu Thr Ala Glu Ile Asp Gln Leu Glu Gln Arg Ala
 1355 1360 1365
 Asp Asn Leu Thr Thr Ile Ala His Glu Leu Gln Gln Tyr Ile Asp
 1370 1375 1380
 Asn Leu Asn Lys Thr Leu Val Asp Leu Asp Trp Leu Asn Arg Ile
 1385 1390 1395
 Glu Thr Tyr Val Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly
 1400 1405 1410
 Leu Val Val Val Phe Cys Ile Pro Leu Leu Leu Phe Cys Cys Leu
 1415 1420 1425
 Ser Thr Gly Phe Cys Gly Cys Phe Gly Cys Val Gly Ser Cys Cys
 1430 1435 1440
 His Ser Leu Cys Ser Arg Arg Gln Phe Glu Thr Tyr Glu Pro Ile
 1445 1450 1455
 Glu Lys Val His Ile His
 1460
 <210> 57
 <211> 1235
 <212> PRT
 <213> Mouse hepatitis virus
 <400> 57
 Met Leu Phe Val Phe Ile Leu Leu Leu Pro Ser Cys Leu Gly Tyr Ile
 1 5 10 15
 Gly Asp Phe Arg Cys Ile Gln Thr Val Asn Tyr Asn Gly Asn Asn Ala
 20 25 30

Ser Ala Pro Ser Ile Ser Thr Glu Ala Val Asp Val Ser Lys Gly Arg
35 40 45

Gly Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Ala Thr Leu Leu
50 55 60

Leu Thr Gly Tyr Tyr Pro Val Asp Gly Ser Asn Tyr Arg Asn Leu Ala
65 70 75 80

Leu Thr Gly Thr Asn Thr Leu Ser Leu Thr Trp Phe Lys Pro Pro Phe
85 90 95

Leu Ser Glu Phe Asn Asp Gly Ile Phe Ala Lys Val Gln Asn Leu Lys
100 105 110

Thr Asn Thr Pro Thr Gly Ala Thr Ser Tyr Phe Pro Thr Ile Val Ile
115 120 125

Gly Ser Leu Phe Gly Asn Thr Ser Tyr Thr Val Val Leu Glu Pro Tyr
130 135 140

Asn Asn Ile Ile Met Ala Ser Val Cys Thr Tyr Thr Ile Cys Gln Leu
145 150 155 160

Pro Tyr Thr Pro Cys Lys Pro Asn Thr Asn Gly Asn Arg Val Ile Gly
165 170 175

Phe Trp His Thr Asp Val Lys Pro Pro Ile Cys Leu Leu Lys Arg Asn
180 185 190

Phe Thr Phe Asn Val Asn Ala Pro Trp Leu Tyr Phe His Phe Tyr Gln
195 200 205

Gln Gly Gly Thr Phe Tyr Ala Tyr Tyr Ala Asp Lys Pro Ser Ala Thr
210 215 220

Thr Phe Leu Phe Ser Val Tyr Ile Gly Asp Ile Leu Thr Gln Tyr Phe
225 230 235 240

Val Leu Pro Phe Ile Cys Thr Pro Thr Ala Gly Ser Thr Leu Ala Pro
245 250 255

Leu Tyr Trp Val Thr Pro Leu Leu Lys Arg Gln Tyr Leu Phe Asn Phe
260 265 270

Asn Glu Lys Gly Val Ile Thr Ser Ala Val Asp Cys Ala Ser Ser Tyr
 275 280 285

Ile Ser Glu Ile Lys Cys Lys Thr Gln Ser Leu Leu Pro Ser Thr Gly
 290 295 300

Val Tyr Asp Leu Ser Gly Tyr Thr Val Gln Pro Val Gly Val Val Tyr
 305 310 315 320

Arg Arg Val Pro Asn Leu Pro Asp Cys Lys Ile Glu Glu Trp Leu Thr
 325 330 335

Ala Lys Ser Val Pro Ser Pro Leu Asn Trp Glu Arg Arg Thr Phe Gln
 340 345 350

Asn Cys Asn Phe Asn Leu Ser Ser Leu Leu Arg Tyr Val Gln Ala Glu
 355 360 365

Ser Leu Ser Cys Asn Asn Ile Asp Ala Ser Lys Val Tyr Gly Met Cys
 370 375 380

Phe Gly Ser Val Ser Val Asp Lys Phe Ala Ile Pro Arg Ser Arg Gln
 385 390 395 400

Ile Asp Leu Gln Ile Gly Asn Ser Gly Phe Leu Gln Thr Ala Asn Tyr
 405 410 415

Lys Ile Asp Thr Ala Ala Thr Ser Cys Gln Leu Tyr Tyr Ser Leu Pro
 420 425 430

Lys Asn Asn Val Thr Ile Asn Asn Tyr Asn Pro Ser Ser Trp Asn Arg
 435 440 445

Arg Tyr Gly Phe Lys Val Asn Asp Arg Cys Gln Ile Phe Ala Asn Ile
 450 455 460

Leu Leu Asn Gly Ile Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln
 465 470 475 480

Leu Pro Asn Thr Glu Val Ala Thr Gly Val Cys Val Arg Tyr Asp Leu
 485 490 495

Tyr Gly Ile Thr Gly Gln Gly Val Phe Lys Glu Val Lys Ala Asp Tyr
 500 505 510

Tyr Asn Ser Trp Gln Ala Leu Leu Tyr Asp Val Asn Gly Asn Leu Asn
515 520 525

Gly Phe Arg Asp Leu Thr Thr Asn Lys Thr Tyr Thr Ile Arg Ser Cys
530 535 540

Tyr Ser Gly Arg Val Ser Ala Ala Tyr His Lys Glu Ala Pro Glu Pro
545 550 555 560

Ala Leu Leu Tyr Arg Asn Ile Asn Cys Ser Tyr Val Phe Thr Asn Asn
565 570 575

Ile Ser Arg Glu Glu Asn Pro Leu Asn Tyr Phe Asp Ser Tyr Leu Gly
580 585 590

Cys Val Val Asn Ala Asp Asn Arg Thr Asp Glu Ala Leu Pro Asn Cys
595 600 605

Asn Leu Arg Met Gly Ala Gly Leu Cys Val Asp Tyr Ser Lys Ser Arg
610 615 620

Arg Ala Arg Arg Ser Val Ser Thr Gly Tyr Arg Leu Thr Thr Phe Glu
625 630 635 640

Pro Tyr Met Pro Met Leu Val Asn Asp Ser Val Gln Ser Val Gly Gly
645 650 655

Leu Tyr Glu Met Gln Ile Pro Thr Asn Phe Thr Ile Gly His His Glu
660 665 670

Glu Phe Ile Gln Ile Arg Ala Pro Lys Val Thr Ile Asp Cys Ala Ala
675 680 685

Phe Val Cys Gly Asp Asn Ala Ala Cys Arg Gln Gln Leu Val Glu Tyr
690 695 700

Gly Ser Phe Cys Asp Asn Val Asn Ala Ile Leu Asn Glu Val Asn Asn
705 710 715 720

Leu Leu Asp Asn Met Gln Leu Gln Val Ala Ser Ala Leu Met Gln Gly
725 730 735

Val Thr Ile Ser Ser Arg Leu Pro Asp Gly Ile Ser Gly Pro Ile Asp
740 745 750

Asp Ile Asn Phe Ser Pro Leu Leu Gly Cys Ile Gly Ser Thr Cys Ala

755 760 765
 Glu Asp Gly Asn Gly Pro Ser Ala Ile Arg Gly Arg Ser Ala Ile Glu
 770 775 780
 Asp Leu Leu Phe Asp Lys Val Lys Leu Ser Asp Val Gly Phe Val Glu
 785 790 795 800
 Ala Tyr Asn Asn Cys Thr Gly Gly Gln Glu Val Arg Asp Leu Leu Cys
 805 810 815
 Val Gln Ser Phe Asn Gly Ile Lys Val Leu Pro Pro Val Leu Ser Glu
 820 825 830
 Ser Gln Ile Ser Gly Tyr Thr Ala Gly Ala Thr Ala Ala Ala Met Phe
 835 840 845
 Pro Pro Trp Thr Ala Ala Ala Gly Val Pro Phe Ser Leu Asn Val Gln
 850 855 860
 Tyr Arg Ile Asn Gly Leu Gly Val Thr Met Asn Val Leu Ser Glu Asn
 865 870 875 880
 Gln Lys Met Ile Ala Ser Ala Phe Asn Asn Ala Leu Gly Ala Ile Gln
 885 890 895
 Glu Gly Phe Asp Ala Thr Asn Ser Ala Leu Gly Lys Ile Gln Ser Val
 900 905 910
 Val Asn Ala Asn Ala Glu Ala Leu Asn Asn Leu Leu Asn Gln Leu Ser
 915 920 925
 Asn Arg Phe Gly Ala Ile Ser Ala Ser Leu Gln Glu Ile Leu Thr Arg
 930 935 940
 Leu Asp Ala Val Glu Ala Lys Ala Gln Ile Asp Arg Leu Ile Asn Gly
 945 950 955 960
 Arg Leu Thr Ala Leu Asn Ala Tyr Ile Ser Lys Gln Leu Ser Asp Ser
 965 970 975
 Thr Leu Ile Lys Phe Ser Ala Ala Gln Ala Ile Glu Lys Val Asn Glu
 980 985 990
 Cys Val Lys Ser Gln Thr Thr Arg Ile Asn Phe Cys Gly Asn Gly Asn
 995 1000 1005

His	Ile	Leu	Ser	Leu	Val	Gln	Asn	Ala	Pro	Tyr	Gly	Leu	Cys	Phe
1010						1015					1020			
Ile	His	Phe	Ser	Tyr	Val	Pro	Thr	Ser	Phe	Lys	Thr	Ala	Asn	Val
1025						1030					1035			
Ser	Pro	Gly	Leu	Cys	Ile	Ser	Gly	Asp	Arg	Gly	Leu	Ala	Pro	Lys
1040						1045					1050			
Ala	Gly	Tyr	Phe	Val	Gln	Asp	Asn	Gly	Glu	Trp	Lys	Phe	Thr	Gly
1055						1060					1065			
Ser	Asn	Tyr	Tyr	Tyr	Pro	Glu	Pro	Ile	Thr	Asp	Lys	Asn	Ser	Val
1070						1075					1080			
Ala	Met	Ile	Ser	Cys	Ala	Val	Asn	Tyr	Thr	Lys	Ala	Pro	Glu	Val
1085						1090					1095			
Phe	Leu	Asn	Asn	Ser	Ile	Pro	Asn	Leu	Pro	Asp	Phe	Lys	Glu	Glu
1100						1105					1110			
Leu	Asp	Lys	Trp	Phe	Lys	Asn	Gln	Thr	Ser	Ile	Ala	Pro	Asp	Leu
1115						1120					1125			
Ser	Leu	Asp	Phe	Glu	Lys	Leu	Asn	Val	Thr	Phe	Leu	Asp	Leu	Thr
1130						1135					1140			
Tyr	Glu	Met	Asn	Arg	Ile	Gln	Asp	Ala	Ile	Lys	Lys	Leu	Asn	Glu
1145						1150					1155			
Ser	Tyr	Ile	Asn	Leu	Lys	Glu	Val	Gly	Thr	Tyr	Glu	Met	Tyr	Val
1160						1165					1170			
Lys	Trp	Pro	Trp	Tyr	Val	Trp	Leu	Leu	Ile	Gly	Leu	Ala	Gly	Val
1175						1180					1185			
Ala	Val	Cys	Val	Leu	Leu	Phe	Phe	Ile	Cys	Cys	Cys	Thr	Gly	Cys
1190						1195					1200			
Gly	Ser	Cys	Cys	Phe	Arg	Lys	Cys	Gly	Ser	Cys	Cys	Asp	Glu	Tyr
1205						1210					1215			
Gly	Gly	His	Gln	Asp	Ser	Ile	Val	Ile	His	Asn	Ile	Ser	Ala	His
1220						1225					1230			

Glu Asp
1235

<210> 58
<211> 1363
<212> PRT
<213> human coronavirus

<400> 58

Met Phe Leu Ile Leu Leu Ile Ser Leu Pro Met Ala Leu Ala Val Ile
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Gly Asp Leu Lys Cys Thr Thr Val Ala Ile Asn Asp Val Asp Thr Gly
20 25 30

Val Pro Ser Thr Ser Thr Asp Ile Val Asp Val Thr Asn Gly Leu Gly
35 40 45

Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr Leu Leu Leu
50 55 60

Asn Gly Tyr Tyr Pro Thr Ser Gly Ser Thr Tyr Arg Asn Met Ala Leu
65 70 75 80

Lys Gly Thr Leu Leu Leu Ser Arg Leu Trp Phe Lys Pro Pro Phe Leu
85 90 95

Ser Asp Phe Ile Asn Gly Ile Phe Ala Lys Val Lys Asn Thr Lys Val
100 105 110

Ile Lys His Gly Val Met Tyr Ser Glu Phe Pro Ala Ile Thr Ile Gly
115 120 125

Ser Thr Phe Val Asn Thr Ser Tyr Ser Val Val Val Gln Pro His Thr
130 135 140

Thr Asn Leu Asp Asn Lys Leu Gln Gly Leu Leu Glu Ile Ser Val Cys
145 150 155 160

Gln Tyr Thr Met Cys Glu Tyr Pro Asn Thr Ile Cys His Pro Asn Leu
165 170 175

Gly Asn Arg Arg Val Glu Leu Trp His Trp Asp Thr Gly Val Val Ser
180 185 190

Cys Leu Tyr Lys Arg Asn Phe Thr Tyr Asp Val Asn Ala Asp Tyr Leu

195 200 205
 Tyr Phe His Phe Tyr Gln Glu Gly Gly Ile Phe Tyr Ala Tyr Phe Thr
 210 215 220
 Asp Thr Gly Val Val Thr Lys Phe Leu Phe Asn Val Tyr Leu Gly Thr
 225 230 235 240
 Val Leu Ser Tyr Tyr Tyr Val Met Pro Leu Thr Cys Asn Ser Ala Met
 245 250 255
 Thr Leu Glu Tyr Trp Val Thr Pro Leu Thr Ser Lys Gln Tyr Leu Leu
 260 265 270
 Ala Phe Asn Gln Asp Gly Val Ile Phe Asn Ala Val Asp Cys Lys Ser
 275 280 285
 Asp Phe Met Ser Glu Ile Lys Cys Lys Thr Leu Ser Ile Ala Pro Ser
 290 295 300
 Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Ile Ala Asp
 305 310 315 320
 Val Tyr Arg Arg Ile Pro Asn Leu Pro Asp Cys Asn Ile Glu Ala Trp
 325 330 335
 Leu Asn Asp Lys Ser Val Pro Ser Pro Leu Asn Trp Glu Arg Lys Thr
 340 345 350
 Phe Ser Asn Cys Asn Phe Asn Met Ser Ser Leu Met Ser Phe Ile Gln
 355 360 365
 Ala Asp Ser Phe Thr Cys Asn Asn Ile Asp Ala Ala Lys Ile Tyr Gly
 370 375 380
 Met Cys Phe Ser Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Gly
 385 390 395 400
 Arg Lys Val Asp Leu Gln Leu Gly Asn Leu Gly Tyr Leu Gln Ser Phe
 405 410 415
 Asn Tyr Arg Ile Asp Thr Thr Ala Thr Ser Cys Gln Leu Tyr Tyr Asn
 420 425 430
 Leu Pro Ala Ala Asn Val Ser Val Ser Arg Phe Asn Pro Ser Ile Trp
 435 440 445

Asn Arg Arg Phe Gly Phe Thr Glu Gln Ser Val Phe Lys Pro Gln Pro
 450 455 460
 Ala Gly Val Phe Thr Asp His Asp Val Val Tyr Ala Gln His Cys Phe
 465 470 475 480
 Lys Ala Pro Thr Asn Phe Cys Pro Cys Lys Leu Asp Gly Ser Leu Cys
 485 490 495
 Val Gly Asn Gly Pro Gly Ile Asp Ala Gly Tyr Lys Asn Ser Gly Ile
 500 505 510
 Gly Thr Cys Pro Ala Gly Thr Asn Tyr Leu Thr Cys His Asn Ala Val
 515 520 525
 Gln Cys Asn Cys Leu Cys Thr Pro Asp Pro Ile Thr Ser Lys Ser Thr
 530 535 540
 Gly Pro Tyr Lys Cys Pro Gln Thr Lys Tyr Leu Val Gly Ile Gly Glu
 545 550 555 560
 His Cys Ser Gly Leu Ala Ile Lys Ser Asp Tyr Cys Gly Gly Asn Pro
 565 570 575
 Cys Thr Cys Gln Pro Gln Ala Phe Leu Gly Trp Ser Val Asp Ser Cys
 580 585 590
 Leu Gln Gly Asp Arg Cys Asn Ile Phe Ala Asn Phe Ile Leu His Asp
 595 600 605
 Val Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln Lys Ser Asn Thr
 610 615 620
 Asp Ile Ile Leu Gly Val Cys Val Asn Tyr Asp Leu Tyr Gly Ile Thr
 625 630 635 640
 Gly Gln Gly Ile Phe Val Glu Val Asn Ala Pro Tyr Tyr Asn Ser Trp
 645 650 655
 Gln Asn Leu Leu Tyr Asp Ser Asn Gly Asn Leu Tyr Gly Phe Arg Asp
 660 665 670
 Tyr Leu Thr Asn Arg Thr Phe Met Ile Arg Ser Cys Tyr Ser Gly Arg
 675 680 685

Val Ser Ala Ala Phe His Ala Asn Ser Ser Glu Pro Ala Leu Leu Phe
 690 695 700
 Arg Asn Ile Lys Cys Asn Tyr Val Phe Asn Asn Thr Leu Ser Arg Gln
 705 710 715 720
 Leu Gln Pro Ile Asn Tyr Phe Asp Ser Tyr Leu Gly Cys Val Val Asn
 725 730 735
 Ala Asp Asn Ser Thr Ala Ser Ala Val Gln Thr Cys Asp Leu Thr Val
 740 745 750
 Gly Ser Gly Tyr Cys Val Asp Tyr Ser Thr Lys Arg Arg Ser Arg Arg
 755 760 765
 Ala Ile Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe Thr Val
 770 775 780
 Asn Ser Val Asn Asp Ser Leu Glu His Val Gly Gly Leu Tyr Glu Ile
 785 790 795 800
 Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Met Glu Glu Phe Ile Gln
 805 810 815
 Thr Ser Ser Pro Lys Val Thr Ile Asp Cys Ser Ala Phe Val Cys Gly
 820 825 830
 Asp Cys Ala Ala Cys Lys Ser Gln Leu Val Glu Tyr Gly Ser Phe Cys
 835 840 845
 Asp Asn Ile Asn Ala Ile Leu Thr Glu Val Asn Glu Leu Leu Asp Thr
 850 855 860
 Thr Gln Leu Gln Val Ala Asn Ser Leu Met Asn Gly Val Thr Leu Ser
 865 870 875 880
 Thr Lys Leu Lys Asp Gly Val Asn Phe Asn Val Asp Asp Val Asn Phe
 885 890 895
 Ser Pro Val Leu Gly Cys Leu Gly Ser Glu Cys Asn Lys Val Ser Ser
 900 905 910
 Arg Ser Ala Ile Glu Asp Leu Leu Phe Ser Lys Val Arg Leu Ser Asp
 915 920 925

Val Gly Phe Val Glu Ala Tyr Asn Asn Cys Thr Gly Gly Ala Gly Ile
 930 935 940

Arg Asp Leu Ile Cys Val Gln Ser Tyr Asn Gly Ile Lys Val Leu Pro
 945 950 955 960

Pro Leu Leu Ser Asp Asn Gln Ile Ser Gly Tyr Thr Leu Ala Ala Thr
 965 970 975

Ser Ala Asn Leu Phe Pro Pro Trp Ser Ala Ala Ala Gly Val Pro Phe
 980 985 990

Tyr Leu Asn Val Gln Tyr Arg Ile Asn Gly Ile Gly Val Thr Met Asp
 995 1000 1005

Val Leu Ser Gln Asn Gln Lys Leu Ile Ala Asn Ala Phe Asn Asn
 1010 1015 1020

Ala Leu Asp Ala Ile Gln Glu Gly Phe Asp Ala Thr Asn Ser Ala
 1025 1030 1035

Leu Val Lys Ile Gln Ala Val Val Asn Ala Asp Ala Glu Ala Leu
 1040 1045 1050

Asn Asn Leu Leu Gln Gln Leu Ser Asn Arg Phe Gly Ala Ile Ser
 1055 1060 1065

Ser Ser Leu Gln Glu Ile Leu Ser Arg Leu Asp Ala Leu Glu Ala
 1070 1075 1080

Gln Ala Gln Ile Asp Arg Leu Ile Asn Gly Arg Leu Thr Ala Leu
 1085 1090 1095

Asp Ala Tyr Val Ser Gln Gln Leu Ser Asp Ser Thr Leu Val Lys
 1100 1105 1110

Phe Ser Ala Ala Gln Ala Met Glu Lys Val Asn Glu Cys Val Lys
 1115 1120 1125

Ser Gln Ser Ser Arg Ile Asn Phe Cys Gly Asn Gly Asn His Ile
 1130 1135 1140

Ile Ser Leu Val Gln Asn Ala Pro Tyr Gly Leu Tyr Phe Ile His
 1145 1150 1155

Phe Ser Tyr Val Pro Thr Lys Tyr Val Thr Ala Lys Val Ser Pro

1160		1165		1170
Gly Leu Cys Ile Ala Gly Asp Arg Gly Ile Ala Pro Lys Ser Gly				
1175		1180		1185
Tyr Phe Val Asn Val Asn Asn Thr Trp Met Phe Thr Gly Ser Arg				
1190		1195		1200
Tyr Tyr Tyr Pro Glu Pro Ile Thr Gly Asn Asn Val Val Val Met				
1205		1210		1215
Ser Thr Cys Ala Val Asn Tyr Thr Lys Ala Pro Asp Val Met Leu				
1220		1225		1230
Asn Ile Ser Thr Pro Asn Leu Pro Asp Phe Lys Glu Glu Leu Asp				
1235		1240		1245
Gln Trp Phe Lys Asn Gln Thr Leu Val Ala Pro Asp Leu Ser Leu				
1250		1255		1260
Asp Tyr Ile Asn Val Thr Phe Leu Asp Leu Gln Asp Glu Met Asn				
1265		1270		1275
Arg Leu Gln Glu Ala Ile Lys Val Leu Asn Gln Ser Tyr Ile Asn				
1280		1285		1290
Leu Lys Asp Ile Gly Thr Tyr Glu Tyr Tyr Val Lys Trp Pro Trp				
1295		1300		1305
Tyr Val Trp Leu Leu Ile Gly Phe Ala Gly Val Ala Met Leu Val				
1310		1315		1320
Leu Leu Phe Phe Ile Cys Cys Cys Thr Gly Cys Gly Thr Ser Cys				
1325		1330		1335
Phe Lys Lys Cys Gly Gly Cys Cys Asp Asp Tyr Thr Gly His Gln				
1340		1345		1350
Glu Leu Val Ile Lys Thr Ser His Glu Gly				
1355		1360		

<210> 59
 <211> 1383
 <212> PRT
 <213> Porcine epidemic diarrhea virus

<400> 59

Met Arg Ser Leu Ile Tyr Phe Trp Leu Leu Leu Pro Val Leu Pro Thr
 1 5 10 15
 Leu Ser Leu Pro Gln Asp Val Thr Arg Cys Gln Ser Thr Thr Asn Phe
 20 25 30
 Arg Arg Phe Phe Ser Lys Phe Asn Val Gln Ala Pro Ala Val Val Val
 35 40 45
 Leu Gly Gly Tyr Leu Pro Ser Met Asn Ser Ser Ser Trp Tyr Cys Gly
 50 55 60
 Thr Gly Ile Glu Thr Ala Ser Gly Val His Gly Ile Phe Leu Ser Tyr
 65 70 75 80
 Ile Asp Ser Gly Gln Gly Phe Glu Ile Gly Ile Ser Gln Glu Pro Phe
 85 90 95
 Asp Pro Ser Gly Tyr Gln Leu Tyr Leu His Lys Ala Thr Asn Gly Asn
 100 105 110
 Thr Asn Ala Thr Ala Arg Leu Arg Ile Cys Gln Phe Pro Asp Asn Lys
 115 120 125
 Thr Leu Gly Pro Thr Val Asn Asp Val Thr Thr Gly Arg Asn Cys Leu
 130 135 140
 Phe Asn Lys Ala Ile Pro Ala Tyr Met Arg Asp Gly Lys Asp Ile Val
 145 150 155 160
 Val Gly Ile Thr Trp Asp Asn Asp Arg Val Thr Val Phe Ala Asp Lys
 165 170 175
 Ile Tyr His Phe Tyr Leu Lys Asn Asp Trp Ser Arg Val Ala Thr Arg
 180 185 190
 Cys Tyr Asn Arg Arg Ser Cys Ala Met Gln Tyr Val Tyr Thr Pro Thr
 195 200 205
 Tyr Tyr Met Leu Asn Val Thr Ser Ala Gly Glu Asp Gly Ile Tyr Tyr
 210 215 220
 Glu Pro Cys Thr Ala Asn Cys Thr Gly Tyr Ala Ala Asn Val Phe Ala
 225 230 235 240

Thr Asp Ser Asn Gly His Ile Pro Glu Gly Phe Ser Phe Asn Asn Trp
 245 250 255

Phe Leu Leu Ser Asn Asp Ser Thr Leu Leu His Gly Lys Val Val Ser
 260 265 270

Asn Gln Pro Leu Leu Val Asn Cys Leu Leu Ala Ile Pro Lys Ile Tyr
 275 280 285

Gly Leu Gly Gln Phe Phe Ser Phe Asn His Thr Met Asp Gly Val Cys
 290 295 300

Asn Gly Ala Ala Val Asp Arg Ala Pro Glu Ala Leu Arg Phe Asn Ile
 305 310 315 320

Asn Asp Thr Ser Val Ile Leu Ala Glu Gly Ser Ile Val Leu His Thr
 325 330 335

Ala Leu Gly Thr Asn Leu Ser Phe Val Cys Ser Asn Ser Ser Asp Pro
 340 345 350

His Leu Ala Ile Phe Ala Ile Pro Leu Gly Ala Thr Glu Val Pro Tyr
 355 360 365

Tyr Cys Phe Leu Lys Val Asp Thr Tyr Asn Ser Thr Val Tyr Lys Phe
 370 375 380

Leu Ala Val Leu Pro Ser Thr Val Arg Glu Ile Val Ile Thr Lys Tyr
 385 390 395 400

Gly Asp Val Tyr Val Asn Gly Phe Gly Tyr Leu His Leu Gly Leu Leu
 405 410 415

Asp Ala Val Thr Ile Tyr Phe Thr Gly His Gly Thr Asp Asp Asp Val
 420 425 430

Ser Gly Phe Trp Thr Ile Ala Ser Thr Asn Phe Val Asp Ala Leu Ile
 435 440 445

Glu Val Gln Gly Thr Ser Ile Gln Arg Ile Leu Tyr Cys Asp Asp Pro
 450 455 460

Val Ser Gln Leu Lys Cys Ser Gln Val Ala Phe Asp Leu Asp Asp Gly
 465 470 475 480

Phe Tyr Pro Ile Ser Ser Arg Asn Leu Leu Ser His Glu Gln Pro Ile

485	490	495
Ser Phe Val Thr Leu Pro Ser Phe Asn Asp His Ser Phe Val Asn Ile 500 505 510		
Thr Val Ser Ala Ala Phe Gly Gly Leu Ser Ser Ala Asn Leu Val Ala 515 520 525		
Ser Asp Thr Thr Ile Asn Gly Phe Ser Ser Phe Cys Val Asp Thr Arg 530 535 540		
Gln Phe Thr Ile Thr Leu Phe Tyr Asn Val Thr Asn Ser Tyr Gly Tyr 545 550 555 560		
Val Ser Lys Ser Gln Asp Ser Asn Cys Pro Phe Thr Leu Gln Ser Val 565 570 575		
Asn Asp Tyr Leu Ser Phe Ser Lys Phe Cys Val Ser Thr Ser Leu Leu 580 585 590		
Ala Gly Ala Cys Thr Ile Asp Leu Phe Gly Tyr Pro Ala Phe Gly Ser 595 600 605		
Gly Val Lys Leu Thr Ser Leu Tyr Phe Gln Phe Thr Lys Gly Glu Leu 610 615 620		
Ile Thr Gly Thr Pro Lys Pro Leu Glu Gly Ile Thr Asp Val Ser Phe 625 630 635 640		
Met Thr Leu Asp Val Cys Thr Lys Tyr Thr Ile Tyr Gly Phe Lys Gly 645 650 655		
Glu Gly Ile Ile Thr Leu Thr Asn Ser Ser Ile Leu Ala Gly Val Tyr 660 665 670		
Tyr Thr Ser Asp Ser Gly Gln Leu Leu Ala Phe Lys Asn Val Thr Ser 675 680 685		
Gly Ala Val Tyr Ser Val Thr Pro Cys Ser Phe Ser Glu Gln Ala Ala 690 695 700		
Tyr Val Asn Asp Asp Ile Val Gly Val Ile Ser Ser Leu Ser Asn Ser 705 710 715 720		
Thr Phe Asn Asn Thr Arg Glu Leu Pro Gly Phe Phe Tyr His Ser Asn 725 730 735		

Asp Gly Ser Asn Cys Thr Glu Pro Val Leu Val Tyr Ser Asn Ile Gly
740 745 750

Val Cys Lys Ser Gly Ser Ile Gly Tyr Val Pro Ser Gln Tyr Gly Gln
755 760 765

Val Lys Ile Ala Pro Thr Val Thr Gly Asn Ile Ser Ile Pro Thr Asn
770 775 780

Phe Ser Met Ser Ile Arg Thr Glu Tyr Leu Gln Leu Tyr Asn Thr Pro
785 790 795 800

Val Ser Val Asp Cys Ala Thr Tyr Val Cys Asn Gly Asn Ser Arg Cys
805 810 815

Lys Gln Leu Leu Thr Gln Tyr Thr Ala Ala Cys Lys Thr Ile Glu Ser
820 825 830

Ala Leu Gln Leu Ser Ala Arg Leu Glu Ser Val Glu Val Asn Ser Met
835 840 845

Leu Thr Ile Ser Glu Glu Ala Leu Gln Leu Ala Thr Ile Ser Ser Phe
850 855 860

Asn Gly Asp Gly Tyr Asn Phe Thr Asn Val Leu Gly Ala Ser Val Tyr
865 870 875 880

Asp Pro Ala Ser Gly Arg Val Val Gln Lys Arg Ser Val Ile Glu Asp
885 890 895

Leu Leu Phe Asn Lys Val Val Thr Asn Gly Leu Gly Thr Val Asp Glu
900 905 910

Asp Tyr Lys Arg Cys Ser Asn Gly Arg Ser Val Ala Asp Leu Val Cys
915 920 925

Ala Gln Tyr Tyr Ser Gly Val Met Val Leu Pro Gly Val Val Asp Ala
930 935 940

Glu Lys Leu His Met Tyr Ser Ala Ser Leu Ile Gly Gly Met Ala Leu
945 950 955 960

Gly Gly Ile Thr Ala Ala Ala Ala Leu Pro Phe Ser Tyr Ala Val Gln
965 970 975

Ala Arg Leu Asn Tyr Leu Ala Leu Gln Thr Asp Val Leu Gln Arg Asn
 980 985 990

Gln Gln Leu Leu Ala Glu Ser Phe Asn Ser Ala Ile Gly Asn Ile Thr
 995 1000 1005

Ser Ala Phe Glu Ser Val Lys Glu Ala Ile Ser Gln Thr Ser Lys
 1010 1015 1020

Gly Leu Asn Thr Val Ala His Ala Leu Thr Lys Val Gln Glu Val
 1025 1030 1035

Val Asn Ser Gln Gly Ser Ala Leu Asn Gln Leu Thr Val Gln Leu
 1040 1045 1050

Gln His Asn Phe Gln Ala Ile Ser Ser Ser Ile Asp Asp Ile Tyr
 1055 1060 1065

Ser Arg Leu Asp Ile Leu Leu Ala Asp Val Gln Val Asp Arg Leu
 1070 1075 1080

Ile Thr Gly Arg Leu Ser Ala Leu Asn Ala Phe Val Ala Gln Thr
 1085 1090 1095

Leu Thr Lys Tyr Thr Glu Val Gln Ala Ser Arg Lys Leu Ala Gln
 1100 1105 1110

Gln Lys Val Asn Glu Cys Val Lys Ser Gln Ser Gln Arg Tyr Gly
 1115 1120 1125

Phe Cys Gly Gly Asp Gly Glu His Ile Phe Ser Leu Val Gln Ala
 1130 1135 1140

Ala Pro Gln Gly Leu Leu Phe Leu His Thr Val Leu Val Pro Gly
 1145 1150 1155

Asp Phe Val Asn Val Leu Ala Ile Ala Gly Leu Cys Val Asn Gly
 1160 1165 1170

Glu Ile Ala Leu Thr Leu Arg Glu Pro Gly Leu Val Leu Phe Thr
 1175 1180 1185

His Glu Leu Gln Thr Tyr Thr Ala Thr Glu Tyr Phe Val Ser Ser
 1190 1195 1200

Arg Arg Met Phe Glu Pro Arg Lys Pro Thr Val Ser Asp Phe Val
1205 1210 1215

Gln Ile Glu Ser Cys Val Val Thr Tyr Val Asn Leu Thr Ser Asp
1220 1225 1230

Gln Leu Pro Asp Val Ile Pro Asp Tyr Ile Asp Val Asn Lys Thr
1235 1240 1245

Leu Asp Glu Ile Leu Ala Ser Leu Pro Asn Arg Thr Gly Pro Ser
1250 1255 1260

Leu Pro Leu Asp Val Phe Asn Ala Thr Tyr Leu Asn Leu Thr Gly
1265 1270 1275

Glu Ile Ala Asp Leu Glu Gln Arg Ser Glu Ser Leu Arg Asn Thr
1280 1285 1290

Thr Glu Glu Leu Arg Ser Leu Ile Asn Asn Ile Asn Asn Thr Leu
1295 1300 1305

Val Asp Leu Glu Trp Leu Asn Arg Val Glu Thr Tyr Ile Lys Trp
1310 1315 1320

Pro Trp Trp Val Trp Leu Ile Ile Val Ile Val Leu Ile Phe Val
1325 1330 1335

Val Ser Leu Leu Val Phe Cys Cys Ile Ser Thr Gly Cys Cys Gly
1340 1345 1350

Cys Cys Gly Cys Cys Gly Ala Cys Phe Ser Gly Cys Cys Arg Gly
1355 1360 1365

Pro Arg Leu Gln Pro Tyr Glu Ala Phe Glu Lys Val His Val Gln
1370 1375 1380

<210> 60

<211> 1349

<212> PRT

<213> porcine hemagglutinating encephalomyelitis virus

<400> 60

Met Phe Phe Ile Leu Leu Ile Ser Leu Pro Ser Ala Phe Ala Val Ile
1 5 10 15

Gly Asp Leu Lys Cys Thr Thr Ser Leu Ile Asn Asp Val Asp Thr Gly
20 25 30

Val Pro Ser Ile Ser Ser Glu Val Val Asp Val Thr Asn Gly Leu Gly
 35 40 45
 Thr Phe Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr Leu Leu Leu
 50 55 60
 Asn Gly Tyr Tyr Pro Ile Ser Gly Ala Thr Phe Arg Asn Met Ala Leu
 65 70 75 80
 Lys Gly Thr Arg Leu Leu Ser Thr Leu Trp Phe Lys Pro Pro Phe Leu
 85 90 95
 Ser Pro Phe Asn Asp Gly Ile Phe Ala Lys Val Lys Asn Ser Arg Phe
 100 105 110
 Ser Lys Asp Gly Val Ile Tyr Ser Glu Phe Pro Ala Ile Thr Ile Gly
 115 120 125
 Ser Thr Phe Val Asn Thr Ser Tyr Ser Ile Val Val Glu Pro His Thr
 130 135 140
 Ser Leu Ile Asn Gly Asn Leu Gln Gly Leu Leu Gln Ile Ser Val Cys
 145 150 155 160
 Gln Tyr Thr Met Cys Glu Tyr Pro His Thr Ile Cys His Pro Asn Leu
 165 170 175
 Gly Asn Gln Arg Ile Glu Leu Trp His Tyr Asp Thr Asp Val Val Ser
 180 185 190
 Cys Leu Tyr Arg Arg Asn Phe Thr Tyr Asp Val Asn Ala Asp Tyr Leu
 195 200 205
 Tyr Phe His Phe Tyr Gln Glu Gly Gly Thr Phe Tyr Ala Tyr Phe Thr
 210 215 220
 Asp Thr Gly Phe Val Thr Lys Phe Leu Phe Lys Leu Tyr Leu Gly Thr
 225 230 235 240
 Val Leu Ser His Tyr Tyr Val Met Pro Leu Thr Cys Asn Ser Ala Leu
 245 250 255
 Ser Leu Glu Tyr Trp Val Thr Pro Leu Thr Thr Arg Gln Phe Leu Leu
 260 265 270

Ala Phe Asp Gln Asp Gly Val Leu Tyr His Ala Val Asp Cys Ala Ser
 275 280 285

Asp Phe Met Ser Glu Ile Met Cys Lys Thr Ser Ser Ile Thr Pro Pro
 290 295 300

Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Val Ala Thr
 305 310 315 320

Val Tyr Arg Arg Ile Pro Asp Leu Pro Asn Cys Asp Ile Glu Ala Trp
 325 330 335

Leu Asn Ser Lys Thr Val Ser Ser Pro Leu Asn Trp Glu Arg Lys Ile
 340 345 350

Phe Ser Asn Cys Asn Phe Asn Met Gly Arg Leu Met Ser Phe Ile Gln
 355 360 365

Ala Asp Ser Phe Gly Cys Asn Asn Ile Asp Ala Ser Arg Leu Tyr Gly
 370 375 380

Met Cys Phe Gly Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Ser
 385 390 395 400

Arg Lys Val Asp Leu Gln Val Gly Lys Ser Gly Tyr Leu Gln Ser Phe
 405 410 415

Asn Tyr Lys Ile Asp Thr Ala Val Ser Ser Cys Gln Leu Tyr Tyr Ser
 420 425 430

Leu Pro Ala Ala Asn Val Ser Val Thr His Tyr Asn Pro Ser Ser Trp
 435 440 445

Asn Arg Arg Tyr Gly Phe Asn Asn Gln Ser Phe Gly Ser Arg Gly Leu
 450 455 460

His Asp Ala Val Tyr Ser Gln Gln Cys Phe Asn Thr Pro Asn Thr Tyr
 465 470 475 480

Cys Pro Cys Arg Thr Ser Gln Cys Ile Gly Gly Ala Gly Thr Gly Thr
 485 490 495

Cys Pro Val Gly Thr Thr Val Arg Lys Cys Phe Ala Ala Val Thr Lys
 500 505 510

Ala Thr Lys Cys Thr Cys Trp Cys Gln Pro Asp Pro Ser Thr Tyr Lys
515 520 525

Gly Val Asn Ala Trp Thr Cys Pro Gln Ser Lys Val Ser Ile Gln Pro
530 535 540

Gly Gln His Cys Pro Gly Leu Gly Leu Val Glu Asp Asp Cys Ser Gly
545 550 555 560

Asn Pro Cys Thr Cys Lys Pro Gln Ala Phe Ile Gly Trp Ser Ser Glu
565 570 575

Thr Cys Leu Gln Asn Gly Arg Cys Asn Ile Phe Ala Asn Phe Ile Leu
580 585 590

Asn Asp Val Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln Gln Gly
595 600 605

Asn Thr Ile Ile Thr Thr Asp Val Cys Val Asn Tyr Asp Leu Tyr Gly
610 615 620

Ile Thr Gly Gln Gly Ile Leu Ile Glu Val Asn Ala Thr Tyr Tyr Asn
625 630 635 640

Ser Trp Gln Asn Leu Leu Tyr Asp Ser Ser Gly Asn Leu Tyr Gly Phe
645 650 655

Arg Asp Tyr Leu Ser Asn Arg Thr Phe Leu Ile Arg Ser Cys Tyr Ser
660 665 670

Gly Arg Val Ser Ala Val Phe His Ala Asn Ser Ser Glu Pro Ala Leu
675 680 685

Met Phe Arg Asn Leu Lys Cys Ser His Val Phe Asn Asn Thr Ile Leu
690 695 700

Arg Gln Ile Gln Leu Val Asn Tyr Phe Asp Ser Tyr Leu Gly Cys Val
705 710 715 720

Val Asn Ala Tyr Asn Asn Thr Ala Ser Ala Val Ser Thr Cys Asp Leu
725 730 735

Thr Val Gly Ser Gly Tyr Cys Val Asp Tyr Val Thr Ala Leu Arg Ser
740 745 750

Arg Arg Ser Phe Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe

755 760 765
 Ala Ala Asn Leu Val Asn Asp Ser Ile Glu Pro Val Gly Gly Leu Tyr
 770 775 780
 Glu Ile Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Leu Glu Glu Phe
 785 790 795 800
 Ile Gln Thr Arg Ser Pro Lys Val Thr Ile Asp Cys Ala Thr Phe Val
 805 810 815
 Cys Gly Asp Tyr Ala Ala Cys Arg Gln Gln Leu Ala Glu Tyr Gly Ser
 820 825 830
 Phe Cys Glu Asn Ile Asn Ala Ile Leu Thr Glu Val Asn Glu Leu Leu
 835 840 845
 Asp Thr Thr Gln Leu Gln Val Ala Asn Ser Leu Met Asn Gly Val Thr
 850 855 860
 Leu Ser Thr Lys Ile Lys Asp Gly Ile Asn Phe Asn Val Asp Asp Ile
 865 870 875 880
 Asn Phe Ser Pro Val Leu Gly Cys Leu Gly Ser Glu Cys Asn Arg Ala
 885 890 895
 Ser Thr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Lys Leu
 900 905 910
 Ser Asp Val Gly Phe Val Gln Ala Tyr Asn Asn Cys Thr Gly Gly Ala
 915 920 925
 Glu Ile Arg Asp Leu Ile Cys Val Gln Ser Tyr Asn Gly Ile Lys Val
 930 935 940
 Leu Pro Pro Leu Leu Ser Glu Asn Gln Ile Ser Gly Tyr Thr Leu Ala
 945 950 955 960
 Ala Thr Ala Ala Ser Leu Phe Pro Pro Trp Thr Ala Ala Ala Gly Val
 965 970 975
 Pro Phe Tyr Leu Asn Val Gln Tyr Arg Ile Asn Gly Leu Gly Val Thr
 980 985 990
 Met Asp Val Leu Ser Gln Asn Gln Lys Leu Ile Ala Ser Ala Phe Asn
 995 1000 1005

Asn Ala Leu Asp Ala Ile Gln Glu Gly Phe Asp Ala Thr Asn Ser
 1010 1015 1020
 Ala Leu Val Lys Ile Gln Ala Val Val Asn Ala Asn Ala Glu Ala
 1025 1030 1035
 Leu Asn Asn Leu Leu Gln Gln Leu Ser Asn Arg Phe Gly Ala Ile
 1040 1045 1050
 Ser Ala Ser Leu Gln Glu Ile Leu Ser Arg Leu Asp Ala Leu Glu
 1055 1060 1065
 Ala Lys Ala Gln Ile Asp Arg Leu Ile Asn Gly Arg Leu Thr Ala
 1070 1075 1080
 Leu Asn Ala Tyr Val Ser Gln Gln Leu Ser Asp Ser Thr Leu Val
 1085 1090 1095
 Lys Phe Ser Ala Ala Gln Ala Ile Glu Lys Val Asn Glu Cys Val
 1100 1105 1110
 Lys Ser Gln Ser Ser Arg Ile Asn Phe Cys Gly Asn Gly Asn His
 1115 1120 1125
 Ile Ile Ser Leu Val Gln Asn Ala Pro Tyr Gly Leu Tyr Phe Ile
 1130 1135 1140
 His Phe Ser Tyr Val Pro Thr Lys Tyr Val Thr Ala Lys Val Ser
 1145 1150 1155
 Pro Gly Leu Cys Ile Ala Gly Asp Ile Gly Ile Ser Pro Lys Ser
 1160 1165 1170
 Gly Tyr Phe Ile Asn Val Asn Asn Ser Trp Met Phe Thr Gly Ser
 1175 1180 1185
 Ser Tyr Tyr Tyr Pro Glu Pro Ile Thr Gln Asn Asn Val Val Val
 1190 1195 1200
 Met Ser Thr Cys Ala Val Asn Tyr Thr Lys Ala Pro Asp Leu Met
 1205 1210 1215
 Leu Asn Thr Ser Thr Pro Asn Leu Pro Asp Phe Lys Glu Glu Leu
 1220 1225 1230

Tyr Gln Trp Phe Lys Asn Gln Ser Ser Val Ala Pro Asp Leu Ser
1235 1240 1245

Leu Asp Tyr Ile Asn Val Thr Phe Leu Asp Leu Gln Asp Glu Met
1250 1255 1260

Asn Arg Leu Gln Glu Ala Ile Lys Val Leu Asn Gln Ser Tyr Ile
1265 1270 1275

Asn Leu Lys Asp Ile Gly Thr Tyr Glu Tyr Tyr Val Lys Trp Pro
1280 1285 1290

Trp Tyr Val Trp Leu Leu Ile Gly Leu Ala Gly Val Ala Met Leu
1295 1300 1305

Val Leu Leu Phe Phe Ile Cys Cys Cys Thr Gly Cys Gly Thr Ser
1310 1315 1320

Cys Phe Lys Lys Cys Gly Gly Cys Cys Asp Asp Tyr Thr Gly His
1325 1330 1335

Gln Glu Phe Val Ile Lys Thr Ser His Asp Asp
1340 1345

<210> 61

<211> 1225

<212> PRT

<213> Porcine respiratory coronavirus

<400> 61

Met Lys Lys Leu Phe Val Val Leu Val Val Met Pro Leu Ile Tyr Gly
1 5 10 15

Asp Lys Phe Pro Thr Ser Val Val Ser Asn Cys Thr Asp Gln Cys Ala
20 25 30

Ser Tyr Val Ala Asn Val Phe Thr Thr Gln Pro Gly Gly Phe Ile Pro
35 40 45

Ser Asp Phe Ser Phe Asn Asn Trp Phe Leu Leu Thr Asn Ser Ser Thr
50 55 60

Leu Val Ser Gly Lys Leu Val Thr Lys Gln Pro Leu Leu Val Asn Cys
65 70 75 80

Leu Trp Pro Val Pro Ser Phe Glu Glu Ala Ala Ser Thr Phe Cys Phe

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Asp Asn Asn Thr Asp Val Tyr Cys Val Arg Ser Asp Gln Phe Ser Val
340 345 350

Tyr Val His Ser Thr Cys Lys Ser Ala Leu Trp Asp Asn Val Phe Lys
355 360 365

Arg Asn Cys Thr Asp Val Leu Asp Ala Thr Ala Val Ile Lys Thr Gly
370 375 380

Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn Tyr Leu Thr Phe Asn
385 390 395 400

Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala Asn Cys Lys Phe Asp
405 410 415

Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val Val Arg Ser Leu Tyr
420 425 430

Val Ile Tyr Glu Glu Gly Asp Ser Ile Val Gly Val Pro Ser Asp Asn
435 440 445

Ser Gly Leu His Asp Leu Ser Val Leu His Leu Asp Ser Cys Thr Asp
450 455 460

Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile Ile Arg Gln Thr Asn
465 470 475 480

Arg Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser Leu Ser Gly Asp Leu
485 490 495

Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile Tyr Ser Val Thr Pro
500 505 510

Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp Gly Thr Ile Val Gly
515 520 525

Ala Ile Thr Ser Ile Asn Ser Glu Leu Leu Gly Leu Thr His Trp Thr
530 535 540

Ile Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr Asn Tyr Thr Asn Asp
545 550 555 560

Lys Thr Arg Gly Thr Pro Ile Asp Ser Asn Asp Val Gly Cys Glu Pro
565 570 575

Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys Asn Gly Ala Leu Val
 580 585 590

Phe Ile Asn Val Thr His Ser Asp Gly Asp Val Gln Pro Ile Ser Thr
 595 600 605

Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile Ser Val Gln Val Glu
 610 615 620

Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile Asp Cys Ser Arg Tyr
 625 630 635 640

Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu Leu Thr Gln Tyr Val
 645 650 655

Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala Met Gly Ala Arg Leu
 660 665 670

Glu Asn Met Glu Val Asp Ser Met Leu Phe Val Ser Glu Asn Ala Leu
 675 680 685

Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Ser Glu Thr Leu Asp Pro
 690 695 700

Ile Tyr Thr Gln Trp Pro Asn Ile Gly Gly Phe Trp Leu Glu Gly Leu
 705 710 715 720

Lys Tyr Ile Leu Pro Ser Asp Asn Ser Lys Arg Lys Tyr Arg Ser Ala
 725 730 735

Ile Glu Asp Leu Leu Phe Ser Lys Val Val Thr Ser Gly Leu Gly Thr
 740 745 750

Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly Tyr Asp Ile Ala Asp
 755 760 765

Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met Val Leu Pro Gly Val
 770 775 780

Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala Ser Leu Ala Gly Gly
 785 790 795 800

Ile Thr Leu Gly Ala Phe Gly Gly Gly Ala Val Ser Ile Pro Phe Ala
 805 810 815

Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala Leu Gln Thr Asp Val
820 825 830

Leu Asn Lys Asn Gln Gln Ile Leu Ala Ser Ala Phe Asn Gln Ala Ile
835 840 845

Gly Asn Ile Thr Gln Ser Phe Gly Lys Val Asn Asp Ala Ile His Gln
850 855 860

Thr Ser Arg Gly Leu Thr Thr Val Ala Lys Ala Leu Ala Lys Val Gln
865 870 875 880

Asp Val Val Asn Thr Gln Gly Gln Ala Leu Arg His Leu Thr Val Gln
885 890 895

Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser Ile Ser Asp Ile Tyr
900 905 910

Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln Val Asp Arg Leu Ile
915 920 925

Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val Ser Gln Thr Leu Thr
930 935 940

Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu Ala Lys Asp Lys Val
945 950 955 960

Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe Gly Phe Cys Gly Asn
965 970 975

Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala Pro Asn Gly Met Ile
980 985 990

Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr Glu Thr Val Thr Ala
995 1000 1005

Trp Ser Gly Ile Cys Ala Leu Asp Gly Asp Arg Thr Phe Gly Leu
1010 1015 1020

Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn Leu Asp Asp
1025 1030 1035

Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg Val Ala
1040 1045 1050

Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu Phe

1055 1060 1065
 Val Asn Thr Thr Val Ser Asp Leu Pro Ser Ile Ile Pro Asp Tyr
 1070 1075 1080
 Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Phe Arg
 1085 1090 1095
 Pro Asn Trp Thr Val Pro Glu Leu Thr Leu Asp Val Phe Asn Ala
 1100 1105 1110
 Thr Tyr Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg
 1115 1120 1125
 Ser Glu Lys Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile
 1130 1135 1140
 Asp Asn Ile Asn Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg
 1145 1150 1155
 Ile Glu Thr Tyr Val Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile
 1160 1165 1170
 Gly Leu Val Val Ile Phe Cys Ile Pro Leu Leu Leu Phe Cys Cys
 1175 1180 1185
 Cys Ser Thr Gly Cys Cys Gly Cys Ile Gly Cys Leu Gly Ser Cys
 1190 1195 1200
 Cys His Ser Ile Phe Ser Arg Arg Gln Phe Glu Asn Tyr Glu Pro
 1205 1210 1215
 Ile Glu Lys Val His Val His
 1220 1225
 <210> 62
 <211> 82
 <212> PRT
 <213> Porcine transmissible gastroenteritis coronavirus
 <400> 62
 Met Thr Phe Pro Arg Ala Leu Thr Val Ile Asp Asp Asn Gly Met Val
 1 5 10 15
 Ile Asn Ile Ile Phe Trp Phe Leu Leu Ile Ile Ile Leu Ile Leu Leu
 20 25 30

Ser Ile Ala Leu Leu Asn Ile Ile Lys Leu Cys Met Val Cys Cys Asn
 35 40 45

Leu Gly Arg Thr Val Ile Ile Val Pro Ala Gln His Ala Tyr Asp Ala
 50 55 60

Tyr Lys Asn Phe Met Arg Ile Lys Ala Tyr Asn Pro Asp Gly Ala Leu
 65 70 75 80

Leu Ala

<210> 63

<211> 4376

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 63

Met Glu Ser Leu Val Leu Gly Val Asn Glu Lys Thr His Val Gln Leu
 1 5 10 15

Ser Leu Pro Val Leu Gln Val Arg Asp Val Leu Val Arg Gly Phe Gly
 20 25 30

Asp Ser Val Glu Glu Ala Leu Ser Glu Ala Arg Glu His Leu Lys Asn
 35 40 45

Gly Thr Cys Gly Leu Val Glu Leu Glu Lys Gly Val Leu Pro Gln Leu
 50 55 60

Glu Gln Pro Tyr Val Phe Ile Lys Arg Ser Asp Ala Leu Ser Thr Asn
 65 70 75 80

His Gly His Lys Val Val Glu Leu Val Ala Glu Met Asp Gly Ile Gln
 85 90 95

Tyr Gly Arg Ser Gly Ile Thr Leu Gly Val Leu Val Pro His Val Gly
 100 105 110

Glu Thr Pro Ile Ala Tyr Arg Asn Val Leu Leu Arg Lys Asn Gly Asn
 115 120 125

Lys Gly Ala Gly Gly His Ser Tyr Gly Ile Asp Leu Lys Ser Tyr Asp
 130 135 140

Leu Gly Asp Glu Leu Gly Thr Asp Pro Ile Glu Asp Tyr Glu Gln Asn

145 150 155 160
 Trp Asn Thr Lys His Gly Ser Gly Ala Leu Arg Glu Leu Thr Arg Glu.
 165 170 175
 Leu Asn Gly Gly Ala Val Thr Arg Tyr Val Asp Asn Asn Phe Cys Gly
 180 185 190
 Pro Asp Gly Tyr Pro Leu Asp Cys Ile Lys Asp Phe Leu Ala Arg Ala
 195 200 205
 Gly Lys Ser Met Cys Thr Leu Ser Glu Gln Leu Asp Tyr Ile Glu Ser
 210 215 220
 Lys Arg Gly Val Tyr Cys Cys Arg Asp His Glu His Glu Ile Ala Trp
 225 230 235 240
 Phe Thr Glu Arg Ser Asp Lys Ser Tyr Glu His Gln Thr Pro Phe Glu
 245 250 255
 Ile Lys Ser Ala Lys Lys Phe Asp Thr Phe Lys Gly Glu Cys Pro Lys
 260 265 270
 Phe Val Phe Pro Leu Asn Ser Lys Val Lys Val Ile Gln Pro Arg Val
 275 280 285
 Glu Lys Lys Lys Thr Glu Gly Phe Met Gly Arg Ile Arg Ser Val Tyr
 290 295 300
 Pro Val Ala Ser Pro Gln Glu Cys Asn Asn Met His Leu Ser Thr Leu
 305 310 315 320
 Met Lys Cys Asn His Cys Asp Glu Val Ser Trp Gln Thr Cys Asp Phe
 325 330 335
 Leu Lys Ala Thr Cys Glu His Cys Gly Thr Glu Asn Leu Val Ile Glu
 340 345 350
 Gly Pro Thr Thr Cys Gly Tyr Leu Pro Thr Asn Ala Val Val Lys Met
 355 360 365
 Pro Cys Pro Ala Cys Gln Asp Pro Glu Ile Gly Pro Glu His Ser Val
 370 375 380
 Ala Asp Tyr His Asn His Ser Asn Ile Glu Thr Arg Leu Arg Lys Gly
 385 390 395 400

Gly Arg Thr Arg Cys Phe Gly Gly Cys Val Phe Ala Tyr Val Gly Cys
 405 410 415

Tyr Asn Lys Arg Ala Tyr Trp Val Pro Arg Ala Ser Ala Asp Ile Gly
 420 425 430

Ser Gly His Thr Gly Ile Thr Gly Asp Asn Val Glu Thr Leu Asn Glu
 435 440 445

Asp Leu Leu Glu Ile Leu Ser Arg Glu Arg Val Asn Ile Asn Ile Val
 450 455 460

Gly Asp Phe His Leu Asn Glu Glu Val Ala Ile Ile Leu Ala Ser Phe
 465 470 475 480

Ser Ala Ser Thr Ser Ala Phe Ile Asp Thr Ile Lys Ser Leu Asp Tyr
 485 490 495

Lys Ser Phe Lys Thr Ile Val Glu Ser Cys Gly Asn Tyr Lys Val Thr
 500 505 510

Lys Gly Lys Pro Val Lys Gly Ala Trp Asn Ile Gly Gln Gln Arg Ser
 515 520 525

Val Leu Thr Pro Leu Cys Gly Phe Pro Ser Gln Ala Ala Gly Val Ile
 530 535 540

Arg Ser Ile Phe Ala Arg Thr Leu Asp Ala Ala Asn His Ser Ile Pro
 545 550 555 560

Asp Leu Gln Arg Ala Ala Val Thr Ile Leu Asp Gly Ile Ser Glu Gln
 565 570 575

Ser Leu Arg Leu Val Asp Ala Met Val Tyr Thr Ser Asp Leu Leu Thr
 580 585 590

Asn Ser Val Ile Ile Met Ala Tyr Val Thr Gly Gly Leu Val Gln Gln
 595 600 605

Thr Ser Gln Trp Leu Ser Asn Leu Leu Gly Thr Thr Val Glu Lys Leu
 610 615 620

Arg Pro Ile Phe Glu Trp Ile Glu Ala Lys Leu Ser Ala Gly Val Glu
 625 630 635 640

Phe Leu Lys Asp Ala Trp Glu Ile Leu Lys Phe Leu Ile Thr Gly Val
645 650 655

Phe Asp Ile Val Lys Gly Gln Ile Gln Val Ala Ser Asp Asn Ile Lys
660 665 670

Asp Cys Val Lys Cys Phe Ile Asp Val Val Asn Lys Ala Leu Glu Met
675 680 685

Cys Ile Asp Gln Val Thr Ile Ala Gly Ala Lys Leu Arg Ser Leu Asn
690 695 700

Leu Gly Glu Val Phe Ile Ala Gln Ser Lys Gly Leu Tyr Arg Gln Cys
705 710 715 720

Ile Arg Gly Lys Glu Gln Leu Gln Leu Leu Met Pro Leu Lys Ala Pro
725 730 735

Lys Glu Val Thr Phe Leu Glu Gly Asp Ser His Asp Thr Val Leu Thr
740 745 750

Ser Glu Glu Val Val Leu Lys Asn Gly Glu Leu Glu Ala Leu Glu Thr
755 760 765

Pro Val Asp Ser Phe Thr Asn Gly Ala Ile Val Gly Thr Pro Val Cys
770 775 780

Val Asn Gly Leu Met Leu Leu Glu Ile Lys Asp Lys Glu Gln Tyr Cys
785 790 795 800

Ala Leu Ser Pro Gly Leu Leu Ala Thr Asn Asn Val Phe Arg Leu Lys
805 810 815

Gly Gly Ala Pro Ile Lys Gly Val Thr Phe Gly Glu Asp Thr Val Trp
820 825 830

Glu Val Gln Gly Tyr Lys Asn Val Arg Ile Thr Phe Glu Leu Asp Glu
835 840 845

Arg Val Asp Lys Val Leu Asn Glu Lys Cys Ser Val Tyr Thr Val Glu
850 855 860

Ser Gly Thr Glu Val Thr Glu Phe Ala Cys Val Val Ala Glu Ala Val
865 870 875 880

Val Lys Thr Leu Gln Pro Val Ser Asp Leu Leu Thr Asn Met Gly Ile
885 890 895

Asp Leu Asp Glu Trp Ser Val Ala Thr Phe Tyr Leu Phe Asp Asp Ala
900 905 910

Gly Glu Glu Asn Phe Ser Ser Arg Met Tyr Cys Ser Phe Tyr Pro Pro
915 920 925

Asp Glu Glu Glu Glu Asp Asp Ala Glu Cys Glu Glu Glu Glu Ile Asp
930 935 940

Glu Thr Cys Glu His Glu Tyr Gly Thr Glu Asp Asp Tyr Gln Gly Leu
945 950 955 960

Pro Leu Glu Phe Gly Ala Ser Ala Glu Thr Val Arg Val Glu Glu Glu
965 970 975

Glu Glu Glu Asp Trp Leu Asp Asp Thr Thr Glu Gln Ser Glu Ile Glu
980 985 990

Pro Glu Pro Glu Pro Thr Pro Glu Glu Pro Val Asn Gln Phe Thr Gly
995 1000 1005

Tyr Leu Lys Leu Thr Asp Asn Val Ala Ile Lys Cys Val Asp Ile
1010 1015 1020

Val Lys Glu Ala Gln Ser Ala Asn Pro Met Val Ile Val Asn Ala
1025 1030 1035

Ala Asn Ile His Leu Lys His Gly Gly Gly Val Ala Gly Ala Leu
1040 1045 1050

Asn Lys Ala Thr Asn Gly Ala Met Gln Lys Glu Ser Asp Asp Tyr
1055 1060 1065

Ile Lys Leu Asn Gly Pro Leu Thr Val Gly Gly Ser Cys Leu Leu
1070 1075 1080

Ser Gly His Asn Leu Ala Lys Lys Cys Leu His Val Val Gly Pro
1085 1090 1095

Asn Leu Asn Ala Gly Glu Asp Ile Gln Leu Leu Lys Ala Ala Tyr
1100 1105 1110

Glu Asn Phe Asn Ser Gln Asp Ile Leu Leu Ala Pro Leu Leu Ser

1115	1120	1125
Ala Gly Ile Phe Gly Ala Lys Pro Leu Gln Ser Leu Gln Val Cys		
1130	1135	1140
Val Gln Thr Val Arg Thr Gln Val Tyr Ile Ala Val Asn Asp Lys		
1145	1150	1155
Ala Leu Tyr Glu Gln Val Val Met Asp Tyr Leu Asp Asn Leu Lys		
1160	1165	1170
Pro Arg Val Glu Ala Pro Lys Gln Glu Glu Pro Pro Asn Thr Glu		
1175	1180	1185
Asp Ser Lys Thr Glu Glu Lys Ser Val Val Gln Lys Pro Val Asp		
1190	1195	1200
Val Lys Pro Lys Ile Lys Ala Cys Ile Asp Glu Val Thr Thr Thr		
1205	1210	1215
Leu Glu Glu Thr Lys Phe Leu Thr Asn Lys Leu Leu Leu Phe Ala		
1220	1225	1230
Asp Ile Asn Gly Lys Leu Tyr His Asp Ser Gln Asn Met Leu Arg		
1235	1240	1245
Gly Glu Asp Met Ser Phe Leu Glu Lys Asp Ala Pro Tyr Met Val		
1250	1255	1260
Gly Asp Val Ile Thr Ser Gly Asp Ile Thr Cys Val Val Ile Pro		
1265	1270	1275
Ser Lys Lys Ala Gly Gly Thr Thr Glu Met Leu Ser Arg Ala Leu		
1280	1285	1290
Lys Lys Val Pro Val Asp Glu Tyr Ile Thr Thr Tyr Pro Gly Gln		
1295	1300	1305
Gly Cys Ala Gly Tyr Thr Leu Glu Glu Ala Lys Thr Ala Leu Lys		
1310	1315	1320
Lys Cys Lys Ser Ala Phe Tyr Val Leu Pro Ser Glu Ala Pro Asn		
1325	1330	1335
Ala Lys Glu Glu Ile Leu Gly Thr Val Ser Trp Asn Leu Arg Glu		
1340	1345	1350

Met Leu Ala His Ala Glu Glu Thr Arg Lys Leu Met Pro Ile Cys
1355 1360 1365

Met Asp Val Arg Ala Ile Met Ala Thr Ile Gln Arg Lys Tyr Lys
1370 1375 1380

Gly Ile Lys Ile Gln Glu Gly Ile Val Asp Tyr Gly Val Arg Phe
1385 1390 1395

Phe Phe Tyr Thr Ser Lys Glu Pro Val Ala Ser Ile Ile Thr Lys
1400 1405 1410

Leu Asn Ser Leu Asn Glu Pro Leu Val Thr Met Pro Ile Gly Tyr
1415 1420 1425

Val Thr His Gly Phe Asn Leu Glu Glu Ala Ala Arg Cys Met Arg
1430 1435 1440

Ser Leu Lys Ala Pro Ala Val Val Ser Val Ser Ser Pro Asp Ala
1445 1450 1455

Val Thr Thr Tyr Asn Gly Tyr Leu Thr Ser Ser Ser Lys Thr Ser
1460 1465 1470

Glu Glu His Phe Val Glu Thr Val Ser Leu Ala Gly Ser Tyr Arg
1475 1480 1485

Asp Trp Ser Tyr Ser Gly Gln Arg Thr Glu Leu Gly Val Glu Phe
1490 1495 1500

Leu Lys Arg Gly Asp Lys Ile Val Tyr His Thr Leu Glu Ser Pro
1505 1510 1515

Val Glu Phe His Leu Asp Gly Glu Val Leu Ser Leu Asp Lys Leu
1520 1525 1530

Lys Ser Leu Leu Ser Leu Arg Glu Val Lys Thr Ile Lys Val Phe
1535 1540 1545

Thr Thr Val Asp Asn Thr Asn Leu His Thr Gln Leu Val Asp Met
1550 1555 1560

Ser Met Thr Tyr Gly Gln Gln Phe Gly Pro Thr Tyr Leu Asp Gly
1565 1570 1575

Ala	Asp	Val	Thr	Lys	Ile	Lys	Pro	His	Val	Asn	His	Glu	Gly	Lys
1580						1585					1590			
Thr	Phe	Phe	Val	Leu	Pro	Ser	Asp	Asp	Thr	Leu	Arg	Ser	Glu	Ala
1595						1600					1605			
Phe	Glu	Tyr	Tyr	His	Thr	Leu	Asp	Glu	Ser	Phe	Leu	Gly	Arg	Tyr
1610						1615					1620			
Met	Ser	Ala	Leu	Asn	His	Thr	Lys	Lys	Trp	Lys	Phe	Pro	Gln	Val
1625						1630					1635			
Gly	Gly	Leu	Thr	Ser	Ile	Lys	Trp	Ala	Asp	Asn	Asn	Cys	Tyr	Leu
1640						1645					1650			
Ser	Ser	Val	Leu	Leu	Ala	Leu	Gln	Gln	Leu	Glu	Val	Lys	Phe	Asn
1655						1660					1665			
Ala	Pro	Ala	Leu	Gln	Glu	Ala	Tyr	Tyr	Arg	Ala	Arg	Ala	Gly	Asp
1670						1675					1680			
Ala	Ala	Asn	Phe	Cys	Ala	Leu	Ile	Leu	Ala	Tyr	Ser	Asn	Lys	Thr
1685						1690					1695			
Val	Gly	Glu	Leu	Gly	Asp	Val	Arg	Glu	Thr	Met	Thr	His	Leu	Leu
1700						1705					1710			
Gln	His	Ala	Asn	Leu	Glu	Ser	Ala	Lys	Arg	Val	Leu	Asn	Val	Val
1715						1720					1725			
Cys	Lys	His	Cys	Gly	Gln	Lys	Thr	Thr	Thr	Leu	Thr	Gly	Val	Glu
1730						1735					1740			
Ala	Val	Met	Tyr	Met	Gly	Thr	Leu	Ser	Tyr	Asp	Asn	Leu	Lys	Thr
1745						1750					1755			
Gly	Val	Ser	Ile	Pro	Cys	Val	Cys	Gly	Arg	Asp	Ala	Thr	Gln	Tyr
1760						1765					1770			
Leu	Val	Gln	Gln	Glu	Ser	Ser	Phe	Val	Met	Met	Ser	Ala	Pro	Pro
1775						1780					1785			
Ala	Glu	Tyr	Lys	Leu	Gln	Gln	Gly	Thr	Phe	Leu	Cys	Ala	Asn	Glu
1790						1795					1800			

Tyr Thr Gly Asn Tyr Gln Cys Gly His Tyr Thr His Ile Thr Ala
 1805 1810 1815
 Lys Glu Thr Leu Tyr Arg Ile Asp Gly Ala His Leu Thr Lys Met
 1820 1825 1830
 Ser Glu Tyr Lys Gly Pro Val Thr Asp Val Phe Tyr Lys Glu Thr
 1835 1840 1845
 Ser Tyr Thr Thr Thr Ile Lys Pro Val Ser Tyr Lys Leu Asp Gly
 1850 1855 1860
 Val Thr Tyr Thr Glu Ile Glu Pro Lys Leu Asp Gly Tyr Tyr Lys
 1865 1870 1875
 Lys Asp Asn Ala Tyr Tyr Thr Glu Gln Pro Ile Asp Leu Val Pro
 1880 1885 1890
 Thr Gln Pro Leu Pro Asn Ala Ser Phe Asp Asn Phe Lys Leu Thr
 1895 1900 1905
 Cys Ser Asn Thr Lys Phe Ala Asp Asp Leu Asn Gln Met Thr Gly
 1910 1915 1920
 Phe Thr Lys Pro Ala Ser Arg Glu Leu Ser Val Thr Phe Phe Pro
 1925 1930 1935
 Asp Leu Asn Gly Asp Val Val Ala Ile Asp Tyr Arg His Tyr Ser
 1940 1945 1950
 Ala Ser Phe Lys Lys Gly Ala Lys Leu Leu His Lys Pro Ile Val
 1955 1960 1965
 Trp His Ile Asn Gln Ala Thr Thr Lys Thr Thr Phe Lys Pro Asn
 1970 1975 1980
 Thr Trp Cys Leu Arg Cys Leu Trp Ser Thr Lys Pro Val Asp Thr
 1985 1990 1995
 Ser Asn Ser Phe Glu Val Leu Ala Val Glu Asp Thr Gln Gly Met
 2000 2005 2010
 Asp Asn Leu Ala Cys Glu Ser Gln Gln Pro Thr Ser Glu Glu Val
 2015 2020 2025
 Val Glu Asn Pro Thr Ile Gln Lys Glu Val Ile Glu Cys Asp Val

2030	2035	2040
Lys Thr Thr Glu Val Val Gly	Asn Val Ile Leu	Lys Pro Ser Asp
2045	2050	2055
Glu Gly Val Lys Val Thr Gln	Glu Leu Gly His	Glu Asp Leu Met
2060	2065	2070
Ala Ala Tyr Val Glu Asn Thr	Ser Ile Thr Ile	Lys Lys Pro Asn
2075	2080	2085
Glu Leu Ser Leu Ala Leu Gly	Leu Lys Thr Ile	Ala Thr His Gly
2090	2095	2100
Ile Ala Ala Ile Asn Ser Val	Pro Trp Ser Lys	Ile Leu Ala Tyr
2105	2110	2115
Val Lys Pro Phe Leu Gly Gln	Ala Ala Ile Thr	Thr Ser Asn Cys
2120	2125	2130
Ala Lys Arg Leu Ala Gln Arg	Val Phe Asn Asn	Tyr Met Pro Tyr
2135	2140	2145
Val Phe Thr Leu Leu Phe Gln	Leu Cys Thr Phe	Thr Lys Ser Thr
2150	2155	2160
Asn Ser Arg Ile Arg Ala Ser	Leu Pro Thr Thr	Ile Ala Lys Asn
2165	2170	2175
Ser Val Lys Ser Val Ala Lys	Leu Cys Leu Asp	Ala Gly Ile Asn
2180	2185	2190
Tyr Val Lys Ser Pro Lys Phe	Ser Lys Leu Phe	Thr Ile Ala Met
2195	2200	2205
Trp Leu Leu Leu Leu Ser Ile	Cys Leu Gly Ser	Leu Ile Cys Val
2210	2215	2220
Thr Ala Ala Phe Gly Val Leu	Leu Ser Asn Phe	Gly Ala Pro Ser
2225	2230	2235
Tyr Cys Asn Gly Val Arg Glu	Leu Tyr Leu Asn	Ser Ser Asn Val
2240	2245	2250
Thr Thr Met Asp Phe Cys Glu	Gly Ser Phe Pro	Cys Ser Ile Cys
2255	2260	2265

Leu Ser Gly Leu Asp Ser Leu Asp Ser Tyr Pro Ala Leu Glu Thr
 2270 2275 2280
 Ile Gln Val Thr Ile Ser Ser Tyr Lys Leu Asp Leu Thr Ile Leu
 2285 2290 2295
 Gly Leu Ala Ala Glu Trp Val Leu Ala Tyr Met Leu Phe Thr Lys
 2300 2305 2310
 Phe Phe Tyr Leu Leu Gly Leu Ser Ala Ile Met Gln Val Phe Phe
 2315 2320 2325
 Gly Tyr Phe Ala Ser His Phe Ile Ser Asn Ser Trp Leu Met Trp
 2330 2335 2340
 Phe Ile Ile Ser Ile Val Gln Met Ala Pro Val Ser Ala Met Val
 2345 2350 2355
 Arg Met Tyr Ile Phe Phe Ala Ser Phe Tyr Tyr Ile Trp Lys Ser
 2360 2365 2370
 Tyr Val His Ile Met Asp Gly Cys Thr Ser Ser Thr Cys Met Met
 2375 2380 2385
 Cys Tyr Lys Arg Asn Arg Ala Thr Arg Val Glu Cys Thr Thr Ile
 2390 2395 2400
 Val Asn Gly Met Lys Arg Ser Phe Tyr Val Tyr Ala Asn Gly Gly
 2405 2410 2415
 Arg Gly Phe Cys Lys Thr His Asn Trp Asn Cys Leu Asn Cys Asp
 2420 2425 2430
 Thr Phe Cys Thr Gly Ser Thr Phe Ile Ser Asp Glu Val Ala Arg
 2435 2440 2445
 Asp Leu Ser Leu Gln Phe Lys Arg Pro Ile Asn Pro Thr Asp Gln
 2450 2455 2460
 Ser Ser Tyr Ile Val Asp Ser Val Ala Val Lys Asn Gly Ala Leu
 2465 2470 2475
 His Leu Tyr Phe Asp Lys Ala Gly Gln Lys Thr Tyr Glu Arg His
 2480 2485 2490

Pro Leu Ser His Phe Val Asn Leu Asp Asn Leu Arg Ala Asn Asn
 2495 2500 2505
 Thr Lys Gly Ser Leu Pro Ile Asn Val Ile Val Phe Asp Gly Lys
 2510 2515 2520
 Ser Lys Cys Asp Glu Ser Ala Ser Lys Ser Ala Ser Val Tyr Tyr
 2525 2530 2535
 Ser Gln Leu Met Cys Gln Pro Ile Leu Leu Leu Asp Gln Ala Leu
 2540 2545 2550
 Val Ser Asp Val Gly Asp Ser Thr Glu Val Ser Val Lys Met Phe
 2555 2560 2565
 Asp Ala Tyr Val Asp Thr Phe Ser Ala Thr Phe Ser Val Pro Met
 2570 2575 2580
 Glu Lys Leu Lys Ala Leu Val Ala Thr Ala His Ser Glu Leu Ala
 2585 2590 2595
 Lys Gly Val Ala Leu Asp Gly Val Leu Ser Thr Phe Val Ser Ala
 2600 2605 2610
 Ala Arg Gln Gly Val Val Asp Thr Asp Val Asp Thr Lys Asp Val
 2615 2620 2625
 Ile Glu Cys Leu Lys Leu Ser His His Ser Asp Leu Glu Val Thr
 2630 2635 2640
 Gly Asp Ser Cys Asn Asn Phe Met Leu Thr Tyr Asn Lys Val Glu
 2645 2650 2655
 Asn Met Thr Pro Arg Asp Leu Gly Ala Cys Ile Asp Cys Asn Ala
 2660 2665 2670
 Arg His Ile Asn Ala Gln Val Ala Lys Ser His Asn Val Ser Leu
 2675 2680 2685
 Ile Trp Asn Val Lys Asp Tyr Met Ser Leu Ser Glu Gln Leu Arg
 2690 2695 2700
 Lys Gln Ile Arg Ser Ala Ala Lys Lys Asn Asn Ile Pro Phe Arg
 2705 2710 2715

Leu Thr Cys Ala Thr Thr Arg Gln Val Val Asn Val Ile Thr Thr
 2720 2725 2730
 Lys Ile Ser Leu Lys Gly Gly Lys Ile Val Ser Thr Cys Phe Lys
 2735 2740 2745
 Leu Met Leu Lys Ala Thr Leu Leu Cys Val Leu Ala Ala Leu Val
 2750 2755 2760
 Cys Tyr Ile Val Met Pro Val His Thr Leu Ser Ile His Asp Gly
 2765 2770 2775
 Tyr Thr Asn Glu Ile Ile Gly Tyr Lys Ala Ile Gln Asp Gly Val
 2780 2785 2790
 Thr Arg Asp Ile Ile Ser Thr Asp Asp Cys Phe Ala Asn Lys His
 2795 2800 2805
 Ala Gly Phe Asp Ala Trp Phe Ser Gln Arg Gly Gly Ser Tyr Lys
 2810 2815 2820
 Asn Asp Lys Ser Cys Pro Val Val Ala Ala Ile Ile Thr Arg Glu
 2825 2830 2835
 Ile Gly Phe Ile Val Pro Gly Leu Pro Gly Thr Val Leu Arg Ala
 2840 2845 2850
 Ile Asn Gly Asp Phe Leu His Phe Leu Pro Arg Val Phe Ser Ala
 2855 2860 2865
 Val Gly Asn Ile Cys Tyr Thr Pro Ser Lys Leu Ile Glu Tyr Ser
 2870 2875 2880
 Asp Phe Ala Thr Ser Ala Cys Val Leu Ala Ala Glu Cys Thr Ile
 2885 2890 2895
 Phe Lys Asp Ala Met Gly Lys Pro Val Pro Tyr Cys Tyr Asp Thr
 2900 2905 2910
 Asn Leu Leu Glu Gly Ser Ile Ser Tyr Ser Glu Leu Arg Pro Asp
 2915 2920 2925
 Thr Arg Tyr Val Leu Met Asp Gly Ser Ile Ile Gln Phe Pro Asn
 2930 2935 2940
 Thr Tyr Leu Glu Gly Ser Val Arg Val Val Thr Thr Phe Asp Ala

2945		2950		2955
Glu Tyr Cys Arg His Gly Thr Cys Glu Arg Ser Glu Val Gly Ile				
2960		2965		2970
Cys Leu Ser Thr Ser Gly Arg Trp Val Leu Asn Asn Glu His Tyr				
2975		2980		2985
Arg Ala Leu Ser Gly Val Phe Cys Gly Val Asp Ala Met Asn Leu				
2990		2995		3000
Ile Ala Asn Ile Phe Thr Pro Leu Val Gln Pro Val Gly Ala Leu				
3005		3010		3015
Asp Val Ser Ala Ser Val Val Ala Gly Gly Ile Ile Ala Ile Leu				
3020		3025		3030
Val Thr Cys Ala Ala Tyr Tyr Phe Met Lys Phe Arg Arg Val Phe				
3035		3040		3045
Gly Glu Tyr Asn His Val Val Ala Ala Asn Ala Leu Leu Phe Leu				
3050		3055		3060
Met Ser Phe Thr Ile Leu Cys Leu Val Pro Ala Tyr Ser Phe Leu				
3065		3070		3075
Pro Gly Val Tyr Ser Val Phe Tyr Leu Tyr Leu Thr Phe Tyr Phe				
3080		3085		3090
Thr Asn Asp Val Ser Phe Leu Ala His Leu Gln Trp Phe Ala Met				
3095		3100		3105
Phe Ser Pro Ile Val Pro Phe Trp Ile Thr Ala Ile Tyr Val Phe				
3110		3115		3120
Cys Ile Ser Leu Lys His Cys His Trp Phe Phe Asn Asn Tyr Leu				
3125		3130		3135
Arg Lys Arg Val Met Phe Asn Gly Val Thr Phe Ser Thr Phe Glu				
3140		3145		3150
Glu Ala Ala Leu Cys Thr Phe Leu Leu Asn Lys Glu Met Tyr Leu				
3155		3160		3165
Lys Leu Arg Ser Glu Thr Leu Leu Pro Leu Thr Gln Tyr Asn Arg				
3170		3175		3180

Tyr Leu Ala Leu Tyr Asn Lys Tyr Lys Tyr Phe Ser Gly Ala Leu
 3185 3190 3195
 Asp Thr Thr Ser Tyr Arg Glu Ala Ala Cys Cys His Leu Ala Lys
 3200 3205 3210
 Ala Leu Asn Asp Phe Ser Asn Ser Gly Ala Asp Val Leu Tyr Gln
 3215 3220 3225
 Pro Pro Gln Thr Ser Ile Thr Ser Ala Val Leu Gln Ser Gly Phe
 3230 3235 3240
 Arg Lys Met Ala Phe Pro Ser Gly Lys Val Glu Gly Cys Met Val
 3245 3250 3255
 Gln Val Thr Cys Gly Thr Thr Thr Leu Asn Gly Leu Trp Leu Asp
 3260 3265 3270
 Asp Thr Val Tyr Cys Pro Arg His Val Ile Cys Thr Ala Glu Asp
 3275 3280 3285
 Met Leu Asn Pro Asn Tyr Glu Asp Leu Leu Ile Arg Lys Ser Asn
 3290 3295 3300
 His Ser Phe Leu Val Gln Ala Gly Asn Val Gln Leu Arg Val Ile
 3305 3310 3315
 Gly His Ser Met Gln Asn Cys Leu Leu Arg Leu Lys Val Asp Thr
 3320 3325 3330
 Ser Asn Pro Lys Thr Pro Lys Tyr Lys Phe Val Arg Ile Gln Pro
 3335 3340 3345
 Gly Gln Thr Phe Ser Val Leu Ala Cys Tyr Asn Gly Ser Pro Ser
 3350 3355 3360
 Gly Val Tyr Gln Cys Ala Met Arg Pro Asn His Thr Ile Lys Gly
 3365 3370 3375
 Ser Phe Leu Asn Gly Ser Cys Gly Ser Val Gly Phe Asn Ile Asp
 3380 3385 3390
 Tyr Asp Cys Val Ser Phe Cys Tyr Met His His Met Glu Leu Pro
 3395 3400 3405

Thr Gly Val His Ala Gly Thr Asp Leu Glu Gly Lys Phe Tyr Gly
 3410 3415 3420
 Pro Phe Val Asp Arg Gln Thr Ala Gln Ala Ala Gly Thr Asp Thr
 3425 3430 3435
 Thr Ile Thr Leu Asn Val Leu Ala Trp Leu Tyr Ala Ala Val Ile
 3440 3445 3450
 Asn Gly Asp Arg Trp Phe Leu Asn Arg Phe Thr Thr Thr Leu Asn
 3455 3460 3465
 Asp Phe Asn Leu Val Ala Met Lys Tyr Asn Tyr Glu Pro Leu Thr
 3470 3475 3480
 Gln Asp His Val Asp Ile Leu Gly Pro Leu Ser Ala Gln Thr Gly
 3485 3490 3495
 Ile Ala Val Leu Asp Met Cys Ala Ala Leu Lys Glu Leu Leu Gln
 3500 3505 3510
 Asn Gly Met Asn Gly Arg Thr Ile Leu Gly Ser Thr Ile Leu Glu
 3515 3520 3525
 Asp Glu Phe Thr Pro Phe Asp Val Val Arg Gln Cys Ser Gly Val
 3530 3535 3540
 Thr Phe Gln Gly Lys Phe Lys Lys Ile Val Lys Gly Thr His His
 3545 3550 3555
 Trp Met Leu Leu Thr Phe Leu Thr Ser Leu Leu Ile Leu Val Gln
 3560 3565 3570
 Ser Thr Gln Trp Ser Leu Phe Phe Phe Val Tyr Glu Asn Ala Phe
 3575 3580 3585
 Leu Pro Phe Thr Leu Gly Ile Met Ala Ile Ala Ala Cys Ala Met
 3590 3595 3600
 Leu Leu Val Lys His Lys His Ala Phe Leu Cys Leu Phe Leu Leu
 3605 3610 3615
 Pro Ser Leu Ala Thr Val Ala Tyr Phe Asn Met Val Tyr Met Pro
 3620 3625 3630

Ala Ser Trp Val Met Arg Ile Met Thr Trp Leu Glu Leu Ala Asp
3635 3640 3645

Thr Ser Leu Ser Gly Tyr Arg Leu Lys Asp Cys Val Met Tyr Ala
3650 3655 3660

Ser Ala Leu Val Leu Leu Ile Leu Met Thr Ala Arg Thr Val Tyr
3665 3670 3675

Asp Asp Ala Ala Arg Arg Val Trp Thr Leu Met Asn Val Ile Thr
3680 3685 3690

Leu Val Tyr Lys Val Tyr Tyr Gly Asn Ala Leu Asp Gln Ala Ile
3695 3700 3705

Ser Met Trp Ala Leu Val Ile Ser Val Thr Ser Asn Tyr Ser Gly
3710 3715 3720

Val Val Thr Thr Ile Met Phe Leu Ala Arg Ala Ile Val Phe Val
3725 3730 3735

Cys Val Glu Tyr Tyr Pro Leu Leu Phe Ile Thr Gly Asn Thr Leu
3740 3745 3750

Gln Cys Ile Met Leu Val Tyr Cys Phe Leu Gly Tyr Cys Cys Cys
3755 3760 3765

Cys Tyr Phe Gly Leu Phe Cys Leu Leu Asn Arg Tyr Phe Arg Leu
3770 3775 3780

Thr Leu Gly Val Tyr Asp Tyr Leu Val Ser Thr Gln Glu Phe Arg
3785 3790 3795

Tyr Met Asn Ser Gln Gly Leu Leu Pro Pro Lys Ser Ser Ile Asp
3800 3805 3810

Ala Phe Lys Leu Asn Ile Lys Leu Leu Gly Ile Gly Gly Lys Pro
3815 3820 3825

Cys Ile Lys Val Ala Thr Val Gln Ser Lys Met Ser Asp Val Lys
3830 3835 3840

Cys Thr Ser Val Val Leu Leu Ser Val Leu Gln Gln Leu Arg Val
3845 3850 3855

Glu Ser Ser Ser Lys Leu Trp Ala Gln Cys Val Gln Leu His Asn

3860		3865		3870
Asp Ile Leu Leu Ala Lys	Asp Thr Thr Glu Ala Phe	Glu Lys Met		
3875	3880	3885		
Val Ser Leu Leu Ser Val	Leu Leu Ser Met Gln Gly	Ala Val Asp		
3890	3895	3900		
Ile Asn Arg Leu Cys Glu	Glu Met Leu Asp Asn Arg	Ala Thr Leu		
3905	3910	3915		
Gln Ala Ile Ala Ser Glu	Phe Ser Ser Leu Pro Ser	Tyr Ala Ala		
3920	3925	3930		
Tyr Ala Thr Ala Gln Glu	Ala Tyr Glu Gln Ala Val	Ala Asn Gly		
3935	3940	3945		
Asp Ser Glu Val Val Leu	Lys Lys Leu Lys Lys	Ser Leu Asn Val		
3950	3955	3960		
Ala Lys Ser Glu Phe Asp	Arg Asp Ala Ala Met Gln	Arg Lys Leu		
3965	3970	3975		
Glu Lys Met Ala Asp Gln	Ala Met Thr Gln Met Tyr	Lys Gln Ala		
3980	3985	3990		
Arg Ser Glu Asp Lys Arg	Ala Lys Val Thr Ser Ala	Met Gln Thr		
3995	4000	4005		
Met Leu Phe Thr Met Leu	Arg Lys Leu Asp Asn Asp	Ala Leu Asn		
4010	4015	4020		
Asn Ile Ile Asn Asn Ala	Arg Asp Gly Cys Val Pro	Leu Asn Ile		
4025	4030	4035		
Ile Pro Leu Thr Thr Ala	Ala Lys Leu Met Val Val	Val Pro Asp		
4040	4045	4050		
Tyr Gly Thr Tyr Lys Asn	Thr Cys Asp Gly Asn Thr	Phe Thr Tyr		
4055	4060	4065		
Ala Ser Ala Leu Trp Glu	Ile Gln Gln Val Val Asp	Ala Asp Ser		
4070	4075	4080		
Lys Ile Val Gln Leu Ser	Glu Ile Asn Met Asp Asn	Ser Pro Asn		
4085	4090	4095		

Leu Ala Trp Pro Leu Ile Val Thr Ala Leu Arg Ala Asn Ser Ala
 4100 4105 4110
 Val Lys Leu Gln Asn Asn Glu Leu Ser Pro Val Ala Leu Arg Gln
 4115 4120 4125
 Met Ser Cys Ala Ala Gly Thr Thr Gln Thr Ala Cys Thr Asp Asp
 4130 4135 4140
 Asn Ala Leu Ala Tyr Tyr Asn Asn Ser Lys Gly Gly Arg Phe Val
 4145 4150 4155
 Leu Ala Leu Leu Ser Asp His Gln Asp Leu Lys Trp Ala Arg Phe
 4160 4165 4170
 Pro Lys Ser Asp Gly Thr Gly Thr Ile Tyr Thr Glu Leu Glu Pro
 4175 4180 4185
 Pro Cys Arg Phe Val Thr Asp Thr Pro Lys Gly Pro Lys Val Lys
 4190 4195 4200
 Tyr Leu Tyr Phe Ile Lys Gly Leu Asn Asn Leu Asn Arg Gly Met
 4205 4210 4215
 Val Leu Gly Ser Leu Ala Ala Thr Val Arg Leu Gln Ala Gly Asn
 4220 4225 4230
 Ala Thr Glu Val Pro Ala Asn Ser Thr Val Leu Ser Phe Cys Ala
 4235 4240 4245
 Phe Ala Val Asp Pro Ala Lys Ala Tyr Lys Asp Tyr Leu Ala Ser
 4250 4255 4260
 Gly Gly Gln Pro Ile Thr Asn Cys Val Lys Met Leu Cys Thr His
 4265 4270 4275
 Thr Gly Thr Gly Gln Ala Ile Thr Val Thr Pro Glu Ala Asn Met
 4280 4285 4290
 Asp Gln Glu Ser Phe Gly Gly Ala Ser Cys Cys Leu Tyr Cys Arg
 4295 4300 4305
 Cys His Ile Asp His Pro Asn Pro Lys Gly Phe Cys Asp Leu Lys
 4310 4315 4320

Gly Lys Tyr Val Gln Ile Pro Thr Thr Cys Ala Asn Asp Pro Val
 4325 4330 4335

Gly Phe Thr Leu Arg Asn Thr Val Cys Thr Val Cys Gly Met Trp
 4340 4345 4350

Lys Gly Tyr Gly Cys Ser Cys Asp Gln Leu Arg Glu Pro Leu Met
 4355 4360 4365

Gln Ser Ala Asp Ala Ser Thr Phe
 4370 4375

<210> 64

<211> 2697

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 64

Phe Lys Arg Val Cys Gly Val Ser Ala Ala Arg Leu Thr Pro Cys Gly
 1 5 10 15

Thr Gly Thr Ser Thr Asp Val Val Tyr Arg Ala Phe Asp Ile Tyr Asn
 20 25 30

Glu Lys Val Ala Gly Phe Ala Lys Phe Leu Lys Thr Asn Cys Cys Arg
 35 40 45

Phe Gln Glu Lys Asp Glu Glu Gly Asn Leu Leu Asp Ser Tyr Phe Val
 50 55 60

Val Lys Arg His Thr Met Ser Asn Tyr Gln His Glu Glu Thr Ile Tyr
 65 70 75 80

Asn Leu Val Lys Asp Cys Pro Ala Val Ala Val His Asp Phe Phe Lys
 85 90 95

Phe Arg Val Asp Gly Asp Met Val Pro His Ile Ser Arg Gln Arg Leu
 100 105 110

Thr Lys Tyr Thr Met Ala Asp Leu Val Tyr Ala Leu Arg His Phe Asp
 115 120 125

Glu Gly Asn Cys Asp Thr Leu Lys Glu Ile Leu Val Thr Tyr Asn Cys
 130 135 140

Cys Asp Asp Asp Tyr Phe Asn Lys Lys Asp Trp Tyr Asp Phe Val Glu

145 150 155 160
 Asn Pro Asp Ile Leu Arg Val Tyr Ala Asn Leu Gly Glu Arg Val Arg
 165 170 175
 Gln Ser Leu Leu Lys Thr Val Gln Phe Cys Asp Ala Met Arg Asp Ala
 180 185 190
 Gly Ile Val Gly Val Leu Thr Leu Asp Asn Gln Asp Leu Asn Gly Asn
 195 200 205
 Trp Tyr Asp Phe Gly Asp Phe Val Gln Val Ala Pro Gly Cys Gly Val
 210 215 220
 Pro Ile Val Asp Ser Tyr Tyr Ser Leu Leu Met Pro Ile Leu Thr Leu
 225 230 235 240
 Thr Arg Ala Leu Ala Ala Glu Ser His Met Asp Ala Asp Leu Ala Lys
 245 250 255
 Pro Leu Ile Lys Trp Asp Leu Leu Lys Tyr Asp Phe Thr Glu Glu Arg
 260 265 270
 Leu Cys Leu Phe Asp Arg Tyr Phe Lys Tyr Trp Asp Gln Thr Tyr His
 275 280 285
 Pro Asn Cys Ile Asn Cys Leu Asp Asp Arg Cys Ile Leu His Cys Ala
 290 295 300
 Asn Phe Asn Val Leu Phe Ser Thr Val Phe Pro Pro Thr Ser Phe Gly
 305 310 315 320
 Pro Leu Val Arg Lys Ile Phe Val Asp Gly Val Pro Phe Val Val Ser
 325 330 335
 Thr Gly Tyr His Phe Arg Glu Leu Gly Val Val His Asn Gln Asp Val
 340 345 350
 Asn Leu His Ser Ser Arg Leu Ser Phe Lys Glu Leu Leu Val Tyr Ala
 355 360 365
 Ala Asp Pro Ala Met His Ala Ala Ser Gly Asn Leu Leu Leu Asp Lys
 370 375 380
 Arg Thr Thr Cys Phe Ser Val Ala Ala Leu Thr Asn Asn Val Ala Phe
 385 390 395 400

Gln Thr Val Lys Pro Gly Asn Phe Asn Lys Asp Phe Tyr Asp Phe Ala
405 410 415

Val Ser Lys Gly Phe Phe Lys Glu Gly Ser Ser Val Glu Leu Lys His
420 425 430

Phe Phe Phe Ala Gln Asp Gly Asn Ala Ala Ile Ser Asp Tyr Asp Tyr
435 440 445

Tyr Arg Tyr Asn Leu Pro Thr Met Cys Asp Ile Arg Gln Leu Leu Phe
450 455 460

Val Val Glu Val Val Asp Lys Tyr Phe Asp Cys Tyr Asp Gly Gly Cys
465 470 475 480

Ile Asn Ala Asn Gln Val Ile Val Asn Asn Leu Asp Lys Ser Ala Gly
485 490 495

Phe Pro Phe Asn Lys Trp Gly Lys Ala Arg Leu Tyr Tyr Asp Ser Met
500 505 510

Ser Tyr Glu Asp Gln Asp Ala Leu Phe Ala Tyr Thr Lys Arg Asn Val
515 520 525

Ile Pro Thr Ile Thr Gln Met Asn Leu Lys Tyr Ala Ile Ser Ala Lys
530 535 540

Asn Arg Ala Arg Thr Val Ala Gly Val Ser Ile Cys Ser Thr Met Thr
545 550 555 560

Asn Arg Gln Phe His Gln Lys Leu Leu Lys Ser Ile Ala Ala Thr Arg
565 570 575

Gly Ala Thr Val Val Ile Gly Thr Ser Lys Phe Tyr Gly Gly Trp His
580 585 590

Asn Met Leu Lys Thr Val Tyr Ser Asp Val Glu Thr Pro His Leu Met
595 600 605

Gly Trp Asp Tyr Pro Lys Cys Asp Arg Ala Met Pro Asn Met Leu Arg
610 615 620

Ile Met Ala Ser Leu Val Leu Ala Arg Lys His Asn Thr Cys Cys Asn
625 630 635 640

Leu Ser His Arg Phe Tyr Arg Leu Ala Asn Glu Cys Ala Gln Val Leu
 645 650 655
 Ser Glu Met Val Met Cys Gly Gly Ser Leu Tyr Val Lys Pro Gly Gly
 660 665 670
 Thr Ser Ser Gly Asp Ala Thr Thr Ala Tyr Ala Asn Ser Val Phe Asn
 675 680 685
 Ile Cys Gln Ala Val Thr Ala Asn Val Asn Ala Leu Leu Ser Thr Asp
 690 695 700
 Gly Asn Lys Ile Ala Asp Lys Tyr Val Arg Asn Leu Gln His Arg Leu
 705 710 715 720
 Tyr Glu Cys Leu Tyr Arg Asn Arg Asp Val Asp His Glu Phe Val Asp
 725 730 735
 Glu Phe Tyr Ala Tyr Leu Arg Lys His Phe Ser Met Met Ile Leu Ser
 740 745 750
 Asp Asp Ala Val Val Cys Tyr Asn Ser Asn Tyr Ala Ala Gln Gly Leu
 755 760 765
 Val Ala Ser Ile Lys Asn Phe Lys Ala Val Leu Tyr Tyr Gln Asn Asn
 770 775 780
 Val Phe Met Ser Glu Ala Lys Cys Trp Thr Glu Thr Asp Leu Thr Lys
 785 790 795 800
 Gly Pro His Glu Phe Cys Ser Gln His Thr Met Leu Val Lys Gln Gly
 805 810 815
 Asp Asp Tyr Val Tyr Leu Pro Tyr Pro Asp Pro Ser Arg Ile Leu Gly
 820 825 830
 Ala Gly Cys Phe Val Asp Asp Ile Val Lys Thr Asp Gly Thr Leu Met
 835 840 845
 Ile Glu Arg Phe Val Ser Leu Ala Ile Asp Ala Tyr Pro Leu Thr Lys
 850 855 860
 His Pro Asn Gln Glu Tyr Ala Asp Val Phe His Leu Tyr Leu Gln Tyr
 865 870 875 880

Ile Arg Lys Leu His Asp Glu Leu Thr Gly His Met Leu Asp Met Tyr
 885 890 895
 Ser Val Met Leu Thr Asn Asp Asn Thr Ser Arg Tyr Trp Glu Pro Glu
 900 905 910
 Phe Tyr Glu Ala Met Tyr Thr Pro His Thr Val Leu Gln Ala Val Gly
 915 920 925
 Ala Cys Val Leu Cys Asn Ser Gln Thr Ser Leu Arg Cys Gly Ala Cys
 930 935 940
 Ile Arg Arg Pro Phe Leu Cys Cys Lys Cys Cys Tyr Asp His Val Ile
 945 950 955 960
 Ser Thr Ser His Lys Leu Val Leu Ser Val Asn Pro Tyr Val Cys Asn
 965 970 975
 Ala Pro Gly Cys Asp Val Thr Asp Val Thr Gln Leu Tyr Leu Gly Gly
 980 985 990
 Met Ser Tyr Tyr Cys Lys Ser His Lys Pro Pro Ile Ser Phe Pro Leu
 995 1000 1005
 Cys Ala Asn Gly Gln Val Phe Gly Leu Tyr Lys Asn Thr Cys Val
 1010 1015 1020
 Gly Ser Asp Asn Val Thr Asp Phe Asn Ala Ile Ala Thr Cys Asp
 1025 1030 1035
 Trp Thr Asn Ala Gly Asp Tyr Ile Leu Ala Asn Thr Cys Thr Glu
 1040 1045 1050
 Arg Leu Lys Leu Phe Ala Ala Glu Thr Leu Lys Ala Thr Glu Glu
 1055 1060 1065
 Thr Phe Lys Leu Ser Tyr Gly Ile Ala Thr Val Arg Glu Val Leu
 1070 1075 1080
 Ser Asp Arg Glu Leu His Leu Ser Trp Glu Val Gly Lys Pro Arg
 1085 1090 1095
 Pro Pro Leu Asn Arg Asn Tyr Val Phe Thr Gly Tyr Arg Val Thr
 1100 1105 1110
 Lys Asn Ser Lys Val Gln Ile Gly Glu Tyr Thr Phe Glu Lys Gly

1115	1120	1125
Asp Tyr Gly Asp Ala Val Val Tyr Arg Gly Thr Thr Thr Tyr Lys		
1130	1135	1140
Leu Asn Val Gly Asp Tyr Phe Val Leu Thr Ser His Thr Val Met		
1145	1150	1155
Pro Leu Ser Ala Pro Thr Leu Val Pro Gln Glu His Tyr Val Arg		
1160	1165	1170
Ile Thr Gly Leu Tyr Pro Thr Leu Asn Ile Ser Asp Glu Phe Ser		
1175	1180	1185
Ser Asn Val Ala Asn Tyr Gln Lys Val Gly Met Gln Lys Tyr Ser		
1190	1195	1200
Thr Leu Gln Gly Pro Pro Gly Thr Gly Lys Ser His Phe Ala Ile		
1205	1210	1215
Gly Leu Ala Leu Tyr Tyr Pro Ser Ala Arg Ile Val Tyr Thr Ala		
1220	1225	1230
Cys Ser His Ala Ala Val Asp Ala Leu Cys Glu Lys Ala Leu Lys		
1235	1240	1245
Tyr Leu Pro Ile Asp Lys Cys Ser Arg Ile Ile Pro Ala Arg Ala		
1250	1255	1260
Arg Val Glu Cys Phe Asp Lys Phe Lys Val Asn Ser Thr Leu Glu		
1265	1270	1275
Gln Tyr Val Phe Cys Thr Val Asn Ala Leu Pro Glu Thr Thr Ala		
1280	1285	1290
Asp Ile Val Val Phe Asp Glu Ile Ser Met Ala Thr Asn Tyr Asp		
1295	1300	1305
Leu Ser Val Val Asn Ala Arg Leu Arg Ala Lys His Tyr Val Tyr		
1310	1315	1320
Ile Gly Asp Pro Ala Gln Leu Pro Ala Pro Arg Thr Leu Leu Thr		
1325	1330	1335
Lys Gly Thr Leu Glu Pro Glu Tyr Phe Asn Ser Val Cys Arg Leu		
1340	1345	1350

Met Lys Thr Ile Gly Pro Asp Met Phe Leu Gly Thr Cys Arg Arg
1355 1360 1365

Cys Pro Ala Glu Ile Val Asp Thr Val Ser Ala Leu Val Tyr Asp
1370 1375 1380

Asn Lys Leu Lys Ala His Lys Asp Lys Ser Ala Gln Cys Phe Lys
1385 1390 1395

Met Phe Tyr Lys Gly Val Ile Thr His Asp Val Ser Ser Ala Ile
1400 1405 1410

Asn Arg Pro Gln Ile Gly Val Val Arg Glu Phe Leu Thr Arg Asn
1415 1420 1425

Pro Ala Trp Arg Lys Ala Val Phe Ile Ser Pro Tyr Asn Ser Gln
1430 1435 1440

Asn Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
1445 1450 1455

Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln
1460 1465 1470

Thr Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val
1475 1480 1485

Ala Ile Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp
1490 1495 1500

Arg Asp Leu Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro
1505 1510 1515

Arg Arg Asn Val Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu
1520 1525 1530

Phe Lys Asp Cys Ser Lys Ile Ile Thr Gly Leu His Pro Thr Gln
1535 1540 1545

Ala Pro Thr His Leu Ser Val Asp Ile Lys Phe Lys Thr Glu Gly
1550 1555 1560

Leu Cys Val Asp Ile Pro Gly Ile Pro Lys Asp Met Thr Tyr Arg
1565 1570 1575

Arg	Leu	Ile	Ser	Met	Met	Gly	Phe	Lys	Met	Asn	Tyr	Gln	Val	Asn
1580						1585					1590			
Gly	Tyr	Pro	Asn	Met	Phe	Ile	Thr	Arg	Glu	Glu	Ala	Ile	Arg	His
1595						1600					1605			
Val	Arg	Ala	Trp	Ile	Gly	Phe	Asp	Val	Glu	Gly	Cys	His	Ala	Thr
1610						1615					1620			
Arg	Asp	Ala	Val	Gly	Thr	Asn	Leu	Pro	Leu	Gln	Leu	Gly	Phe	Ser
1625						1630					1635			
Thr	Gly	Val	Asn	Leu	Val	Ala	Val	Pro	Thr	Gly	Tyr	Val	Asp	Thr
1640						1645					1650			
Glu	Asn	Asn	Thr	Glu	Phe	Thr	Arg	Val	Asn	Ala	Lys	Pro	Pro	Pro
1655						1660					1665			
Gly	Asp	Gln	Phe	Lys	His	Leu	Ile	Pro	Leu	Met	Tyr	Lys	Gly	Leu
1670						1675					1680			
Pro	Trp	Asn	Val	Val	Arg	Ile	Lys	Ile	Val	Gln	Met	Leu	Ser	Asp
1685						1690					1695			
Thr	Leu	Lys	Gly	Leu	Ser	Asp	Arg	Val	Val	Phe	Val	Leu	Trp	Ala
1700						1705					1710			
His	Gly	Phe	Glu	Leu	Thr	Ser	Met	Lys	Tyr	Phe	Val	Lys	Ile	Gly
1715						1720					1725			
Pro	Glu	Arg	Thr	Cys	Cys	Leu	Cys	Asp	Lys	Arg	Ala	Thr	Cys	Phe
1730						1735					1740			
Ser	Thr	Ser	Ser	Asp	Thr	Tyr	Ala	Cys	Trp	Asn	His	Ser	Val	Gly
1745						1750					1755			
Phe	Asp	Tyr	Val	Tyr	Asn	Pro	Phe	Met	Ile	Asp	Val	Gln	Gln	Trp
1760						1765					1770			
Gly	Phe	Thr	Gly	Asn	Leu	Gln	Ser	Asn	His	Asp	Gln	His	Cys	Gln
1775						1780					1785			
Val	His	Gly	Asn	Ala	His	Val	Ala	Ser	Cys	Asp	Ala	Ile	Met	Thr
1790						1795					1800			

Arg Cys	Leu Ala Val His Glu	Cys Phe Val Lys Arg	Val Asp Trp
1805	1810	1815	
Ser Val	Glu Tyr Pro Ile Ile	Gly Asp Glu Leu Arg	Val Asn Ser
1820	1825	1830	
Ala Cys	Arg Lys Val Gln His	Met Val Val Lys Ser	Ala Leu Leu
1835	1840	1845	
Ala Asp	Lys Phe Pro Val Leu	His Asp Ile Gly Asn	Pro Lys Ala
1850	1855	1860	
Ile Lys	Cys Val Pro Gln Ala	Glu Val Glu Trp Lys	Phe Tyr Asp
1865	1870	1875	
Ala Gln	Pro Cys Ser Asp Lys	Ala Tyr Lys Ile Glu	Glu Leu Phe
1880	1885	1890	
Tyr Ser	Tyr Ala Thr His His	Asp Lys Phe Thr Asp	Gly Val Cys
1895	1900	1905	
Leu Phe	Trp Asn Cys Asn Val	Asp Arg Tyr Pro Ala	Asn Ala Ile
1910	1915	1920	
Val Cys	Arg Phe Asp Thr Arg	Val Leu Ser Asn Leu	Asn Leu Pro
1925	1930	1935	
Gly Cys	Asp Gly Gly Ser Leu	Tyr Val Asn Lys His	Ala Phe His
1940	1945	1950	
Thr Pro	Ala Phe Asp Lys Ser	Ala Phe Thr Asn Leu	Lys Gln Leu
1955	1960	1965	
Pro Phe	Phe Tyr Tyr Ser Asp	Ser Pro Cys Glu Ser	His Gly Lys
1970	1975	1980	
Gln Val	Val Ser Asp Ile Asp	Tyr Val Pro Leu Lys	Ser Ala Thr
1985	1990	1995	
Cys Ile	Thr Arg Cys Asn Leu	Gly Gly Ala Val Cys	Arg His His
2000	2005	2010	
Ala Asn	Glu Tyr Arg Gln Tyr	Leu Asp Ala Tyr Asn	Met Met Ile
2015	2020	2025	
Ser Ala	Gly Phe Ser Leu Trp	Ile Tyr Lys Gln Phe	Asp Thr Tyr

2030	2035	2040
Asn Leu Trp Asn Thr Phe Thr 2045	Arg Leu Gln Ser 2050	Leu Glu Asn Val 2055
Ala Tyr Asn Val Val Asn Lys 2060	Gly His Phe Asp 2065	Gly His Ala Gly 2070
Glu Ala Pro Val Ser Ile Ile 2075	Asn Asn Ala Val 2080	Tyr Thr Lys Val 2085
Asp Gly Ile Asp Val Glu Ile 2090	Phe Glu Asn Lys 2095	Thr Thr Leu Pro 2100
Val Asn Val Ala Phe Glu Leu 2105	Trp Ala Lys Arg 2110	Asn Ile Lys Pro 2115
Val Pro Glu Ile Lys Ile Leu 2120	Asn Asn Leu Gly 2125	Val Asp Ile Ala 2130
Ala Asn Thr Val Ile Trp Asp 2135	Tyr Lys Arg Glu 2140	Ala Pro Ala His 2145
Val Ser Thr Ile Gly Val Cys 2150	Thr Met Thr Asp 2155	Ile Ala Lys Lys 2160
Pro Thr Glu Ser Ala Cys Ser 2165	Ser Leu Thr Val 2170	Leu Phe Asp Gly 2175
Arg Val Glu Gly Gln Val Asp 2180	Leu Phe Arg Asn 2185	Ala Arg Asn Gly 2190
Val Leu Ile Thr Glu Gly Ser 2195	Val Lys Gly Leu 2200	Thr Pro Ser Lys 2205
Gly Pro Ala Gln Ala Ser Val 2210	Asn Gly Val Thr 2215	Leu Ile Gly Glu 2220
Ser Val Lys Thr Gln Phe Asn 2225	Tyr Phe Lys Lys 2230	Val Asp Gly Ile 2235
Ile Gln Gln Leu Pro Glu Thr 2240	Tyr Phe Thr Gln 2245	Ser Arg Asp Leu 2250
Glu Asp Phe Lys Pro Arg Ser 2255	Gln Met Glu Thr 2260	Asp Phe Leu Glu 2265

Leu	Ala	Met	Asp	Glu	Phe	Ile	Gln	Arg	Tyr	Lys	Leu	Glu	Gly	Tyr
2270						2275					2280			
Ala	Phe	Glu	His	Ile	Val	Tyr	Gly	Asp	Phe	Ser	His	Gly	Gln	Leu
2285						2290					2295			
Gly	Gly	Leu	His	Leu	Met	Ile	Gly	Leu	Ala	Lys	Arg	Ser	Gln	Asp
2300						2305					2310			
Ser	Pro	Leu	Lys	Leu	Glu	Asp	Phe	Ile	Pro	Met	Asp	Ser	Thr	Val
2315						2320					2325			
Lys	Asn	Tyr	Phe	Ile	Thr	Asp	Ala	Gln	Thr	Gly	Ser	Ser	Lys	Cys
2330						2335					2340			
Val	Cys	Ser	Val	Ile	Asp	Leu	Leu	Leu	Asp	Asp	Phe	Val	Glu	Ile
2345						2350					2355			
Ile	Lys	Ser	Gln	Asp	Leu	Ser	Val	Ile	Ser	Lys	Val	Val	Lys	Val
2360						2365					2370			
Thr	Ile	Asp	Tyr	Ala	Glu	Ile	Ser	Phe	Met	Leu	Trp	Cys	Lys	Asp
2375						2380					2385			
Gly	His	Val	Glu	Thr	Phe	Tyr	Pro	Lys	Leu	Gln	Ala	Ser	Gln	Ala
2390						2395					2400			
Trp	Gln	Pro	Gly	Val	Ala	Met	Pro	Asn	Leu	Tyr	Lys	Met	Gln	Arg
2405						2410					2415			
Met	Leu	Leu	Glu	Lys	Cys	Asp	Leu	Gln	Asn	Tyr	Gly	Glu	Asn	Ala
2420						2425					2430			
Val	Ile	Pro	Lys	Gly	Ile	Met	Met	Asn	Val	Ala	Lys	Tyr	Thr	Gln
2435						2440					2445			
Leu	Cys	Gln	Tyr	Leu	Asn	Thr	Leu	Thr	Leu	Ala	Val	Pro	Tyr	Asn
2450						2455					2460			
Met	Arg	Val	Ile	His	Phe	Gly	Ala	Gly	Ser	Asp	Lys	Gly	Val	Ala
2465						2470					2475			
Pro	Gly	Thr	Ala	Val	Leu	Arg	Gln	Trp	Leu	Pro	Thr	Gly	Thr	Leu
2480						2485					2490			

Leu Val Asp Ser Asp Leu Asn Asp Phe Val Ser Asp Ala Asp Ser
 2495 2500 2505
 Thr Leu Ile Gly Asp Cys Ala Thr Val His Thr Ala Asn Lys Trp
 2510 2515 2520
 Asp Leu Ile Ile Ser Asp Met Tyr Asp Pro Arg Thr Lys His Val
 2525 2530 2535
 Thr Lys Glu Asn Asp Ser Lys Glu Gly Phe Phe Thr Tyr Leu Cys
 2540 2545 2550
 Gly Phe Ile Lys Gln Lys Leu Ala Leu Gly Gly Ser Ile Ala Val
 2555 2560 2565
 Lys Ile Thr Glu His Ser Trp Asn Ala Asp Leu Tyr Lys Leu Met
 2570 2575 2580
 Gly His Phe Ser Trp Trp Thr Ala Phe Val Thr Asn Val Asn Ala
 2585 2590 2595
 Ser Ser Ser Glu Ala Phe Leu Ile Gly Ala Asn Tyr Leu Gly Lys
 2600 2605 2610
 Pro Lys Glu Gln Ile Asp Gly Tyr Thr Met His Ala Asn Tyr Ile
 2615 2620 2625
 Phe Trp Arg Asn Thr Asn Pro Ile Gln Leu Ser Ser Tyr Ser Leu
 2630 2635 2640
 Phe Asp Met Ser Lys Phe Pro Leu Lys Leu Arg Gly Thr Ala Val
 2645 2650 2655
 Met Ser Leu Lys Glu Asn Gln Ile Asn Asp Met Ile Tyr Ser Leu
 2660 2665 2670
 Leu Glu Lys Gly Arg Leu Ile Ile Arg Glu Asn Asn Arg Val Val
 2675 2680 2685
 Val Ser Ser Asp Ile Leu Val Asn Asn
 2690 2695

<210> 65

<211> 274

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 65

Met Asp Leu Phe Met Arg Phe Phe Thr Leu Arg Ser Ile Thr Ala Gln
 1 5 10 15

Pro Val Lys Ile Asp Asn Ala Ser Pro Ala Ser Thr Val His Ala Thr
 20 25 30

Ala Thr Ile Pro Leu Gln Ala Ser Leu Pro Phe Gly Trp Leu Val Ile
 35 40 45

Gly Val Ala Phe Leu Ala Val Phe Gln Ser Ala Thr Lys Ile Ile Ala
 50 55 60

Leu Asn Lys Arg Trp Gln Leu Ala Leu Tyr Lys Gly Phe Gln Phe Ile
 65 70 75 80

Cys Asn Leu Leu Leu Leu Phe Val Thr Ile Tyr Ser His Leu Leu Leu
 85 90 95

Val Ala Ala Gly Met Glu Ala Gln Phe Leu Tyr Leu Tyr Ala Leu Ile
 100 105 110

Tyr Phe Leu Gln Cys Ile Asn Ala Cys Arg Ile Ile Met Arg Cys Trp
 115 120 125

Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu Tyr Asp Ala Asn
 130 135 140

Tyr Phe Val Cys Trp His Thr His Asn Tyr Asp Tyr Cys Ile Pro Tyr
 145 150 155 160

Asn Ser Val Thr Asp Thr Ile Val Val Thr Glu Gly Asp Gly Ile Ser
 165 170 175

Thr Pro Lys Leu Lys Glu Asp Tyr Gln Ile Gly Gly Tyr Ser Glu Asp
 180 185 190

Arg His Ser Gly Val Lys Asp Tyr Val Val Val His Gly Tyr Phe Thr
 195 200 205

Glu Val Tyr Tyr Gln Leu Glu Ser Thr Gln Ile Thr Thr Asp Thr Gly
 210 215 220

Ile Glu Asn Ala Thr Phe Phe Ile Phe Asn Lys Leu Val Lys Asp Pro
 225 230 235 240

Pro Asn Val Gln Ile His Thr Ile Asp Gly Ser Ser Gly Val Ala Asn
 245 250 255

Pro Ala Met Asp Pro Ile Tyr Asp Glu Pro Thr Thr Thr Thr Ser Val
 260 265 270

Pro Leu

<210> 66
 <211> 154
 <212> PRT
 <213> Severe acute respiratory syndrome virus
 <400> 66

Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
 1 5 10 15

Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu Ser Leu Leu Lys Val
 20 25 30

Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr Thr Lys Leu Val Val
 35 40 45

Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr Met Ser Leu Tyr Met
 50 55 60

Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser Leu His Lys Leu Leu
 65 70 75 80

Gln Thr Leu Val Leu Lys Met Leu His Ser Ser Ser Leu Thr Ser Leu
 85 90 95

Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln Ser Thr Ala Leu Gln
 100 105 110

Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met Met Ser Arg Arg Arg
 115 120 125

Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val Ser Thr Asn Leu Cys
 130 135 140

Thr His Ser Phe Arg Lys Lys Gln Val Arg
 145 150

<210> 67
 <211> 63
 <212> PRT
 <213> Severe acute respiratory syndrome virus
 <400> 67

Met Phe His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile
 1 5 10 15

Ile Ile Met Arg Thr Phe Arg Ile Ala Ile Trp Asn Leu Asp Val Ile
 20 25 30

Ile Ser Ser Ile Val Arg Gln Leu Phe Lys Pro Leu Thr Lys Lys Asn
 35 40 45

Tyr Ser Glu Leu Asp Asp Glu Glu Pro Met Glu Leu Asp Tyr Pro
 50 55 60

<210> 68
 <211> 122
 <212> PRT
 <213> Severe acute respiratory syndrome virus
 <400> 68

Met Lys Ile Ile Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu
 1 5 10 15

Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys
 20 25 30

Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro
 35 40 45

Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala
 50 55 60

Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg
 65 70 75 80

Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu
 85 90 95

Leu Tyr Ser Pro Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile
 100 105 110

Leu Cys Phe Thr Ile Lys Arg Lys Thr Glu
 115 120

<210> 69
 <211> 44
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 69

Met Asn Glu Leu Thr Leu Ile Asp Phe Tyr Leu Cys Phe Leu Ala Phe
 1 5 10 15

Leu Leu Phe Leu Val Leu Ile Met Leu Ile Ile Phe Trp Phe Ser Leu
 20 25 30

Glu Ile Gln Asp Leu Glu Glu Pro Cys Thr Lys Val
 35 40

<210> 70
 <211> 39
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 70

Met Lys Leu Leu Ile Val Leu Thr Cys Ile Ser Leu Cys Ser Cys Ile
 1 5 10 15

Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His Val Leu Glu
 20 25 30

Asp Pro Cys Lys Val Gln His
 35

<210> 71
 <211> 84
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 71

Met Cys Leu Lys Ile Leu Val Arg Tyr Asn Thr Arg Gly Asn Thr Tyr
 1 5 10 15

Ser Thr Ala Trp Leu Cys Ala Leu Gly Lys Val Leu Pro Phe His Arg
 20 25 30

Trp His Thr Met Val Gln Thr Cys Thr Pro Asn Val Thr Ile Asn Cys
 35 40 45

Gln Asp Pro Ala Gly Gly Ala Leu Ile Ala Arg Cys Trp Tyr Leu His
 50 55 60

Glu Gly His Gln Thr Ala Ala Phe Arg Asp Val Leu Val Val Leu Asn
 65 70 75 80

Lys Arg Thr Asn

<210> 72
 <211> 98
 <212> PRT
 <213> Severe acute respiratory syndrome virus
 <400> 72

Met Asp Pro Asn Gln Thr Asn Val Val Pro Pro Ala Leu His Leu Val
 1 5 10 15

Asp Pro Gln Ile Gln Leu Thr Ile Thr Arg Met Glu Asp Ala Met Gly
 20 25 30

Gln Gly Gln Asn Ser Ala Asp Pro Lys Val Tyr Pro Ile Ile Leu Arg
 35 40 45

Leu Gly Ser Gln Leu Ser Leu Ser Met Ala Arg Arg Asn Leu Asp Ser
 50 55 60

Leu Glu Ala Arg Ala Phe Gln Ser Thr Pro Ile Val Val Gln Met Thr
 65 70 75 80

Lys Leu Ala Thr Thr Glu Glu Leu Pro Asp Glu Phe Val Val Val Thr
 85 90 95

Ala Lys

<210> 73
 <211> 70
 <212> PRT
 <213> Severe acute respiratory syndrome virus
 <400> 73

Met Leu Pro Pro Cys Tyr Asn Phe Leu Lys Glu Gln His Cys Gln Lys
 1 5 10 15

Ala Ser Thr Gln Arg Glu Ala Glu Ala Ala Val Lys Pro Leu Leu Ala
 20 25 30

Pro His His Val Val Ala Val Ile Gln Glu Ile Gln Leu Leu Ala Ala
 35 40 45

Val Gly Glu Ile Leu Leu Leu Glu Trp Leu Ala Glu Val Val Lys Leu
 50 55 60

Pro Ser Arg Tyr Cys Cys
 65 70

<210> 74
 <211> 6
 <212> RNA
 <213> Coronavirus

<400> 74
 cuaaac

6

<210> 75
 <211> 13
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 75

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly
 1 5 10

<210> 76
 <211> 23
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 76

Thr Ile Pro Leu Gln Ala Ser Leu Pro Phe Gly Trp Leu Val Ile Gly
 1 5 10 15

Val Ala Phe Leu Ala Val Phe
 20

<210> 77
 <211> 23
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 77

Phe Gln Phe Ile Cys Asn Leu Leu Leu Leu Phe Val Thr Ile Tyr Ser
 1 5 10 15

His Leu Leu Leu Val Ala Ala
 20

<210> 78

<211> 23
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 78

Ala Gln Phe Leu Tyr Leu Tyr Ala Leu Ile Tyr Phe Leu Gln Cys Ile
1 5 10 15

Asn Ala Cys Arg Ile Ile Met
20

<210> 79
<211> 18
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 79

Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
1 5 10 15

Ile Leu

<210> 80
<211> 23
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 80

Leu Leu Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp
1 5 10 15

Ile Met Leu Leu Gln Phe Ala
20

<210> 81
<211> 23
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 81

Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe Val
1 5 10 15

Leu Ala Ala Val Tyr Arg Ile
20

<210> 82
<211> 23

<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 82

Gly Gly Ile Ala Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu
1 5 10 15

Ser Tyr Phe Val Ala Ser Phe
20

<210> 83
<211> 20
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 83

His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile Ile Ile
1 5 10 15

Met Arg Thr Phe
20

<210> 84
<211> 15
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 84

Met Lys Ile Ile Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys
1 5 10 15

<210> 85
<211> 19
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 85

Ser Pro Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile Leu Cys
1 5 10 15

Phe Thr Ile

<210> 86
<211> 83
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 86

Glu Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu
 1 5 10 15

Lys Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His
 20 25 30

Pro Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe
 35 40 45

Ala Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala
 50 55 60

Arg Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln
 65 70 75 80

Glu Leu Tyr

<210> 87
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 87
 caggaaacag ctatgacacc aagaacaagg ctctcca

37

<210> 88
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 88
 caggaaacag ctatgacgat agggcctctt ccacaga

37

<210> 89
 <211> 496
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> n is a, c, g, or t

<400> 89
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60

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tttaaáatct gtgtagctgt cgctcggctg catgcctagt gcacctacgc agtataaaca      120
ataataaatt ttactgtcgt tgacaagaaa cgagtaactc gtccctcttc tgcagactgc      180
ttacggtttc gtccgtgttg cagtogatca tcagcatacc taggtttcgt ccgggtgtga      240
ccgaaággta agatggagag ccttgttctt ggtgtcaacg agaaaacaca cgtccaactc      300
agtttgectg tccttcaggt tagagacgtg ctagtgcgtg gcttcgggga ctctgtggaa      360
gaggccctat cggaggcacg tgaacacctc aaaaatggca cttgtggtct agtagagctg      420
gaaaaaggcg tactgcccc a gttgaacag cctatgtgt tcattaaacg ttctgatgcc      480
ttaagcacca atcacg                                         496

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<210> 90

<211> 523

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 90

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gtcgacaaca atttctgtgg ccagatggg taccctcttg attgcatcaa agattttctc      60
gcacgcgcgg gcaagtcaat gtgcactctt tccgaacaac ttgattacat cgagtcgaag      120
agagggtgtct actgctgcgc tgaccatgag catgaaattg cctggttcac tgagcgctct      180
gataagagct acgagcacca gacacccttc gaaáttaaga gtgccaagaa atttgacact      240
ttcaaagggg aatgcccaaa gtttgtgttt cctcttaact caaaagtcaa agtcattcaa      300
ccacgtgttg aaaagaaaaa gactgagggt ttcattggggc gtatacgtc tgggtaccct      360
gttgcatctc cácaggagtg taacaatatg cacttgctta ccttgatgaa atgtaatcat      420
tgcatgaag ttctatggca gacgtgcgcac ttctgaaag ccacttgatga acattgtggc      480
actgaaaatt tagttattga aggacctact acatgtgggt acc                                         523

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<210> 91

<211> 324

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 91

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cttaggtgac gagcttggca ctgatcccat tgaagattat gaacaaaact ggaacactaa      60
gcatggcagt ggtgcactcc gtgaactcac tcgtgagctc aatggagggt cagtcactcg      120
ctatgtcgac aacaatttct gtggcccaga tgggtaccct cttgattgca tcaaagattt      180
tctcgcacgc gcgggcaagt caatgtgcac tctttccgaa caacttgatt acatcgagtc      240
gaagagaggt gtctactgct gccgtgacca tgagcatgaa attgcctggt tcaactgagcg      300
ctcctgataa gagctacgag cacc                                         324

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<210> 92
 <211> 495
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 92
 tgctataata agcgtgccta ctgggttcct cgtgctagtg ctgatattgg gctcaggcca 60
 tactggcatt actggtgaca atgtggagac cttgaatgag gatctccttg agatactgag 120
 tcgtgaacgt gttaacatta acattgttgg cgattttcat ttgaatgaag aggttgccat 180
 cattttggca tctttctctg cttctacaag tgcctttatt gacactataa agagtcttga 240
 ttacaagtct ttcaaaacca ttgttgagtc ctgcggtaac tataaagtta ccaagggaaa 300
 gcccgtaaaa ggtgcttggg acattggaca acagagatca gttttaacac cactgtgtgg 360
 ttttcctca caggctgctg gtgttatcag atcaattttt gcgcgcacac ttgatgcagc 420
 aaaccactca attcctgatt tgcaaagagc agctgtcacc atacttgatg gtatttctga 480
 acagtcatta cgtct 495

<210> 93
 <211> 486
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 93
 gccactcaaa cattgaaact cgactccgca agggaggtag gactagatgt tttggaggct 60
 gtgtgtttgc ctatgttggc tgctataata agcgtgccta ctgggttcct cgtgctagtg 120
 ctgatattgg ctcaggccat actggcatta ctggtgacaa tgtggagacc ttgaatgagg 180
 atctccttga gatactgagt cgtgaacgtg ttaacattaa cattgttggc gattttcatt 240
 tgaatgaaga ggttgccatc attttggcat ctttctctgc ttctacaagt gcctttattg 300
 aactataaaa gagtcttgat tacaagtctt tcaaaaccat tgttgagtcc tgcggtaact 360
 ataaagttac caagggaaaag cccgtaaaag gtgcttggaa cattggacaa cagagatcag 420
 ttttaacacc actgtgtggt tttccctcac aggtctgtgg tggtatcaga tcaatttttg 480
 cgcgca 486

<210> 94
 <211> 567
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 94
 cactactgtg gaaaaactca ggcctatctt tgaatggatt gaggcgaaac ttagtgcagg 60
 agttgaattt ctcaaggatg cttgggagat tctcaaattt ctcattacag gtgtttttga 120

catcgtcaag ggtcaaatac aggttgcttc agataacatc aaggattgtg taaaatgctt 180
cattgatgtt gttaacaagg cactcgaaat gtgcattgat caagtcacta tcgctggcgc 240
aaagttgcga tcaactcaact taggtgaagt cttcatcgct caaagcaagg gactttaccg 300
tcagtgtata cgtggcaagg agcagctgca actactcatg cctcttaagg caccaaaaaga 360
agtaaccttt cttgaagggtg attcacatga cacagtactt acctctgagg aggttggttct 420
caagaacggt gaactcgaag cactcgagac gcccgttgat agcttcacaa atggagctat 480
cgttggcaca ccagtctgtg taaatggcct catgctctta gagattaagg acaagaaca 540
atactgagca ttgtctcctg gtttact 567

<210> 95

<211> 516

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 95

gggagattct caaatttctc attacagggt tttttgacat cgtcaagggt caaatacagg 60
ttgcttcaga taacatcaag gattgtgtaa aatgcttcat tgatgttggt aacaaggcac 120
tcgaaatgtg cattgatcaa gtactatcg ctggcgcaaa gttgcgatca ctcaacttag 180
gtgaagtctt catcgctcaa agcaaggagc tttaccgtca gtgtatacgt ggcaaggagc 240
agctgcaact actcatgctt ctttaaggcac caaagaagt aacctttctt gaagggtgatt 300
cacatgacac agtacttacc tctgaggagg ttgtttctca gaacggtgaa ctogaagcac 360
tcgagacgcc cgttgatagc ttcacaaatg gagctatcgt tggcacacca gtctgtgtaa 420
atggcctcat gctcttagag attaaggaca aagaacaata ctgcgcattg tctcctgggt 480
tactggctac aaacaatgtc tttcgcttaa aagggg 516

<210> 96

<211> 448

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 96

agttcgagtt gaggaagaag aagaggaaga ctggctggat gatactactg agcaatcaga 60
gattgagcca gaaccagaac ctacacctga agaaccagtt aatcagttta ctgggttattt 120
aaaacttact gacaatgttg ccattaaatg tgttgacatc gtttaaggagg cacaaagtgc 180
taatcctatg gtgattgtaa atgctgctaa catacacctg aaacatgggtg gtgggtgtagc 240
aggtgcactc aacaaggcaa ccaatgggtgc catgcaaaag gagagtgatg attacattaa 300
gctaaatggc cctcttacag taggagggtc ttgtttgctt tctggacata atcttgctaa 360
gaagtgtctg catgttggtg gacctaacct aaatgcaggt gaggacatcc agcttcttaa 420

ggcagcatat gaaaattttca attcacag

448

<210> 97

<211> 333

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 97

agaggatgat tatcaagggtc tccctctgga atttgggtgcc tcagctgaaa cagttcgagt 60

tgaggaagaa gaagaggaag actgggtgga tgatactact gagcaatcag agattgagcc 120

agaaccagaa cctacacctg aagaaccagt taatcagttt actgggttatt taaaacttac 180

tgacaatgtt gccattaat gtgttgacat cgtaaggag gcacaaagtg ctaatcctat 240

ggtgattgta aatgctgcta acatacacct gaaacatggt ggtggtgtag caggtgcact 300

caacaaggca accaatggtg ccatgcaaaa gga 333

<210> 98

<211> 399

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 98

gagatgctct caagagcttt gaagaaagtg ccagttgatg agtatataac cacgtaccct 60

ggacaaggat gtgctgggta tacacttgag gaagctaaga ctgctcttaa gaaatgcaaa 120

tctgcatttt atgtactacc ttcagaagca cctaattgcta aggaagagat totaggaact 180

gtatcctgga atttgagaga aatgcttgct catgctgaag agacaagaaa attaattgct 240

atatgcatgg atgttagagc cataatggca accatccaac gtaagtataa aggaattaaa 300

attcaagagg gcatcggtga ctatggtgtc cgattcttct tttatactag taaagagcct 360

gtagcttcta ttattacgaa gctgaactct ctaaattgag 399

<210> 99

<211> 437

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 99

agaaatctgt cgtacagaag cctgtcgatg tgaagccaaa aattaaggcc tgcattgatg 60

aggttaccac aacctggaa gaaactaagt ttcttaccaa taagttactc ttgtttgctg 120

atatcaatgg taagctttac catgattctc agaacatgct tagaggtgaa gatatgtctt 180

tccttgagaa ggatgcacct tacatggtag gtgatgttat cactagtggg gatatacctt 240

gtgttgtaat accctccaaa aaggctgggtg gcactactga gatgctctca agagctttga 300

agaaagtgcc agttgatgag tatataacca cgtaccctgg acaaggatgt gctgggtata 360

cacttgagga agctaagact gctcttaaga aatgcaaata tgcattttat gtactacctt 420
cagaagcacc taatgct 437

<210> 100
<211> 569
<212> DNA
<213> Severe acute respiratory syndrome virus

<400> 100
cctctatcgt attgacggag ctacaccttac aaagatgtca gactacaaag gaccagtgc 60
tgatgttttc tacaaggaaa catcttacac tacaaccatc aagcctgtgt cgtataaact 120
cgatggagtt acttacacag agattgaacc aaaattggat ggggtattata aaaaggataa 180
tgcttactat acagagcagc ctatagacct tgtaccaact caaccattac caaatgcgag 240
ttttgataat ttcaaactca catgttctaa cacaaaattt gctgatgatt taaatcaaat 300
gacaggcttc acaaagccag cttcacgaga gctatctgtc acattcttcc cagacttgaa 360
tggcgatgta gtggctattg actatagaca ctattcagcg agtttcaaga aagggtgctaa 420
attactgcat aagccaattg tttggcacat taaccaggct acaaccaaga caacgttcaa 480
accaaacact tgggtgtttac gttgtctttg gactacaaag ccagtagata cttcaaattc 540
atttgaagtt ctggcagtag aagacacat 569

<210> 101
<211> 187
<212> DNA
<213> Severe acute respiratory syndrome virus

<400> 101
tcagcagata cttcaaattc atttgaagtt ctggcagtag aagacacaca aggaatggac 60
aatcttgctt gtgaaagtca acaaccacc tctgaagaag tagtggaata tctaccata 120
cagaaggaag tcatagagcg tgacgtgaaa actaccgaag ttgtaggcaa tgtcatactt 180
aaaccat 187

<210> 102
<211> 271
<212> DNA
<213> Severe acute respiratory syndrome virus

<400> 102
aaatgcgacg agtctgcttc taagtctgct tctgtgtact acagtcagct gatgtgcaa 60
cctattctgt tgcttgacca agctcttgta tcagacgttg gagatagtag tgaagtttcc 120
gttaagatgt ttgatgctta tgcgacacc ttttcagcaa cttttagtgt tctatggaa 180
aaacttaagg cacttggtgc tacagctcac agcgagtag caaagggtgt agctttagat 240

ggtgtccttt ctacattcgt gtcagctgcc c

271

<210> 103

<211> 363

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 103

catttcatca gcaattcttg gctcatgtgg tttatcatta gtattgtaca aatggcaccc 60

gtttctgcaa tggtaggat gtacatcttc ttgtcttctt tctactacat atggaagagc 120

tatgttcata tcatggatgg ttgcacotct tcgacttgca tgatgtgcta taagcgcaat 180

cgtgccacac gcgttgagtg tacaactatt gttaatggca tgaagagatc tttctatgtc 240

tatgcaaata gaggcogtgg cttctgcaag actcacaatt ggaattgtct caattgtgac 300

acattttgca ctggtagtac attcattagt gatgaagttg ctcgagattt gtcactccag 360

ttt 363

<210> 104

<211> 500

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 104

agagatcttg gcgcatgtat tgactgtaat gcaaggcata tcaatgccca aggtagcaaa 60

aagtcacaat gtttcaactca tctggaatgt aaaagactac atgtctttat ctgaacagct 120

gcgtaaacaa attcgtagtg ctgccaagaa gaacaacata ctttttagac taacttgtgc 180

tacaactaga caggttgtca atgtcataac tactaaaatc tcaactcaagg gtggttaagat 240

tgtagtagtact tgtttttaaac ttatgcttaa ggccacatta ttgtgcgttc ttgctgcatt 300

ggtttgttat atcgttatgc cagtacatac attgtcaatc catgatgggt acacaaatga 360

aatcattgggt tacaaagcca ttcaggatgg tgtcactcgt gacatcattt ctactgatga 420

ttgttttgca aataaacatg ctggttttga cgcattggtt agccagcgtg gtggttcata 480

caaaaatgac aaaagctgcc 500

<210> 105

<211> 537

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 105

cattgtcaat ccatgatgggt tacacaaatg aaatcattgg ttacaaagcc attcaggatg 60

gtgtcactcg tgacatcatt tctactgatg attgttttgc aaataaacat gctggttttg 120

acgcattggt tagccagcgt ggtggttcat acaaaaatga caaaagctgc cctgtagtag 180

ctgctatcat tacaagagag attggtttca tagtgcttgg cttaccgggt actgtgctga 240
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 tttgctacac accttccaaa ctcatlgagt atagtgattt tgctacctct gcttgcgctc 360
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 aactaatttt gctagagggt tctatttctt atagtgagct tgcgccagac actcgttatg 480
 tgcttatgga tggttccatc atacagtttc ctaacactta cctggagggg tctgtta 537

<210> 106

<211> 427

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 106

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 tcttggctca ccttcaatgg ttggccatgt tttctcctat tgtgcctttt tggataacag 180
 caatctatgt attctgtatt tctctgaagc actgccattg gttctttaac aactatctta 240
 ggaaaagagt catgtttaat ggagttacat ttagtacctt cgaggaggct gctttgtgta 300
 cctttttgct caacaaggaa atgtacctaa aattgcgtag cgagacactg ttgccactta 360
 cacagtataa caggtatctt gctctatata acaagtacaa gtatttcagt ggagccttag 420
 atactac 427

<210> 107

<211> 537

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 107

agtaacaact ttgatgctg agtactgtag acatgggtaca tgcgaaaggc cagaagtagg 60
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 aggagttttc tgtggtgttg atgcgatgaa tctcatagct aacatcttta ctctcttgt 180
 gcaacctgtg ggtgcttttag atgtgtctgc ttcagtagtg gctgggtgga ttattgccat 240
 attggtgact tgtgctgcct actactttat gaaattcaga cgtgtttttg gtgagtacaa 300
 ccatgttggt gctgctaatt cacttttgtt ttgatgtct ttcactatac tctgtctggg 360
 accagcttac agctttctgc cgggagtcta ctacgtcttt tacttgtact tgacattcta 420
 tttaccaat gatgtttcat tcttggctca ccttcaatgg ttggccatgt tttctcctat 480
 tgtgcctttt tggataacag caatctatgt attctgtatt tctctgaagc actgcca 537

<210> 108
 <211> 551
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 108
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 agatctgctc attcgcaaat ccaaccatag ctttcttggt caggctggca atgttcaact 120
 tcgtgttatt ggccattcta tgcaaaattg tctgcttagg cttaaagttg atacttctaa 180
 ccctaagaca cccaagtata aatttgtocg tatccaacct ggtcaaacat tttcagttct 240
 agcatgctac aatgggtcac catctggtgt ttatcagtgt gccatgagac ctaatcatac 300
 cattaaaggt tctttcctta atggatcatg tggtagtggt ggttttaaca ttgattatga 360
 ttgctgtctt ttctgctata tgcatacat ggagcttcca acaggagtac acgctggtag 420
 tgacttagaa ggtaaattct atgggtccatt tgttgacaga caaactgcac aggctgcagg 480
 tacagacaca accataacat taaatgtttt ggcattggctg tatgctgctg ttatcaatgg 540
 tgataggtgg t 551

<210> 109
 <211> 593
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 109
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 cacagacatc aatcacttct gctgttctgc agagtgggtt taggaaaatg gcattcccg 120
 caggcaaagt tgaaggggtc atggtacaag taacctgtgg aactacaact cttaatggat 180
 tgtgggttga tgacacagta tactgtocaa gacatgtcat ttgcacagca gaagacatgc 240
 ttaatcctaa ctatgaagat ctgctcattc gcaaatacaa ccatagcttt cttgttcagg 300
 ctggcaatgt tcaacttcgt gttattggcc attctatgca aaattgtctg cttaggctta 360
 aagttgatac ttctaaccct aagacaccca agtataaatt tgtccgtatc caacctggctc 420
 aaacattttc agttctagca tgctacaatg gttcaccatc tgggtgttat cagtgtgcca 480
 tgagacctaa tcataccatt aaaggttctt tccttaatgg atcatgtggt agtgttggtt 540
 ttaacattga ttatgattgc gtgtctttct gctatatgca tcatatggag ctt 593

<210> 110
 <211> 504
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 110

tgtgctgctt tgaagagct gctgcagaat gggatatgaat ggtcgtacta tccttggttag	60
cactatttta gaagatgagt ttacaccatt tgatgttggt agacaatgct ctgggtgttac	120
cttccaaggg taagttcaag aaaattgtta agggcactca tcattggatg cttttaactt	180
tcttgacatc actattgatt cttgttcaaa gtacacagtg gtcactgttt ttctttgttt	240
acgagaatgc tttcttgcca tttactcttg gtattatggc aattgctgca tgtgctatgc	300
tgcttggtta gcataagcac gcattcttgt gcttgtttct gttaccttct cttgcaacag	360
ttgcttactt taatatggtc tacatgcctg ctagctgggt gatgcgtatc atgacatggc	420
ttgaattggc tgacactagc ttgtctggtt ataggcttaa ggatttgttt atgtatgctt	480
cagctttagt tttgcttatt ctca	504

<210> 111

<211> 298

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 111

taggcttaag gatttgttta tgtatgcttc agctttagtt ttgcttattc tcatgacagc	60
tcgcactgtt tatgatgatg ctgctagacg tgtttggaca ctgatgaatg tcattacact	120
tgtttacaaa gtctactatg gtaatgcttt agatcaagct atttccatgt gggccttagt	180
tatttctgta acctctaaact attctgggtg cgttacgact atcatgtttt tagctagagc	240
tatagtgttt gtgtgtgttg agtattaccc attgttattt attacctggc aacacctt	298

<210> 112

<211> 530

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 112

aaacaggcaa gatctgagga caagagggca aaagtaacta gtgctatgca aacaatgctc	60
ttcactatgc ttaggaagct tgataatgat gcacttaaca acattatcaa caatgcgcgt	120
gatggttgtg ttccaotcaa catcatacca ttgactacag cagccaaact catggttgtt	180
gtccctgatt atggtaccta caagaacact tgtgatggta acacctttac atatgcatct	240
gcactctggg aaatccagca agttgttgat gcggatagca agattgttca acttagtgaa	300
attaacatgg acaattcacc aaatttggct tggcctctta ttgttacagc tctaagagcc	360
aactcagctg ttaaaactaca gaataatgaa ctgagtccag tagcactacg acagatgtcc	420
tgtgcggctg gtaccacaca aacagcttgt actgatgaca atgcacttgc ctactataac	480
aattcgaagg gaggtagggt tgtgctggca ttactatcag accaccaagc	530

<210> 113
 <211> 605
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 113
 gaagtcgttc tcaaaaagtt aaagaaatct ttgaatgtgg ctaaactctga gtttgaccgt 60
 gatgctgcca tgcaacgcaa gttggaaaag atggcagatc aggctatgac ccaaattgtac 120
 aaacaggcaa gatctgagga caagagggca aaagtaacta gtgctatgca aacaatgctc 180
 ttcactatgc ttaggaagct tgataatgat gcacttaaca acattatcaa caatgcgcgt 240
 gatggttgtg ttccactcaa catcatacca ttgactacag cagccaaact catggttgtt 300
 gtccctgatt atggtaccta caagaacact tgtgatggta acacctttac atatgcatct 360
 gcactctggg aaatccagca agttgttgat gcggatagca agattgttca acttagtgaa 420
 attaacatgg acaattcacc aaatttggct tggcctotta ttgttacagc totaagagcc 480
 aactcagctg ttaaaactaca gaataatgaa ctgagtccag tagcactacg acagatgtcc 540
 tgtgcggctg gtaccacaca aacagcttgt actgatgaca atgcacttgc ctactataac 600
 aattc 605

<210> 114
 <211> 176
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 114
 aacttggtac aggacaggca attactgtaa caccagaagc taacatggac caagagtcct 60
 ttggtggtgc ttcattgtgt ctgtattgta gatgccacat tgaccatcca aatcctaaag 120
 gattctgtga cttgaaaggt aagtacgtcc aaatacctac cacttgtgct aatgat 176

<210> 115
 <211> 516
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 115
 actgtaacac cagaagctaa catggaccaa gagtcctttg gtggtgcttc atgttgtctg 60
 tattgtagat gccacattga ccatccaaat cctaaaggat tctgtgactt gaaaggtaag 120
 tacgtccaaa tacctaccac ttgtgctaata gaccagtggt gttttacact tagaaacaca 180
 gtctgtaccg tctgcggaat gtggaaaggt tatggctgta gttgtgacca actccgcgaa 240
 cccttgatgc agtctgcgga tgcacaaacg tttttaaacg ggtttgcggt gtaagtgcag 300
 cccgtcttac accgtgcggc acaggcacta gtactgatgt cgtctacagg gcttttgata 360
 tttaacaaga aaaagttgct ggttttgcaa agttcctaaa aactaattgc tgtcgcttcc 420

aggagaagga tgaggaaggc aaattattag actottactt tgtagttaag aggcatacta 480
 tgtctaccta ccaacatgaa gagactattt ataact 516

<210> 116
 <211> 366
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 116
 accacttatt aagtgggatt tgctgaaata tgattttacg gaagagagac tttgtctctt 60
 cgaccgttat tttaaataatt gggaccagac ataccatccc aattgtatta actgttttga 120
 tgataggtgt atccttcatt gtgcaaaactg taatgtgtta ttttctgctg tgtttccacg 180
 tacaagtttt ggaccactag taagaaaaat atttgtagat ggtgttcctt ttgttgtttc 240
 aactggatac cattttcgtg agttaggagt cgtacataat caggatgtaa acttacatag 300
 ctgcgctctc agtttcaagg aacttttagt gtatgctgct gatccagcta tgcattgcagc 360
 ttctgg 366

<210> 117
 <211> 291
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 117
 tgaaaaagtt gctggttttg caaagttcct aaaaactaat tgctgtcgct tccaggagaa 60
 ggatgaggaa ggcaatttat tagactctta ctttgtagtt aagaggcata ctatgtctaa 120
 ctaccaacat gaagagacta ttataaactt ggttaaagat tgtccagcgg ttgctgtcca 180
 tgactttttc aagtttagag tagatggtga catggtacca catatatcac gtcagcgtct 240
 aactaaatac acaatggctg atttagtcta tgctctacgt cattttgatg a 291

<210> 118
 <211> 480
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 118
 gagtcccata tggatgctga tctcgcaaaa ccacttatta agtgggattt gctgaaatat 60
 gattttacgg aagagagact ttgtctcttc gaccgttatt tttaaatttg ggaccagaca 120
 taccatcca attgtattaa ctgtttggat gataggtgta tccttcattg tgcaaaacttt 180
 aatgtgttat tttctactgt gtttccacct acaagttttg gaccactagt aagaaaaata 240
 tttgtagatg gtgttccttt tgttgtttca actggatacc attttcgtga gttaggagtc 300
 gtacataatc aggatgtaaa ctacatagc tcgcgctctca gtttcaagga acttttagtg 360

tatgctgctg atccagctat gcatgcagct tctggcaatt tattgctaga taaacgcact 420
 acatgctttt cagtagctgc actaacaac aatgttgctt ttcaaactgt caaaccgggt 480

<210> 119
 <211> 405
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 119
 aatgggaact ggtacgattt cggtagattc gtacaagtag caccaggctg cggagttcct 60
 attgtggatt catattactc attgctgatg cccatcctca ctttgactag ggcattggct 120
 gctgagtccc atatggatgc tgatctcgca aaaccactta ttaagtgaga ttgctgaaa 180
 tatgatttta cggaagagag actttgtctc ttcgaccgtt attttaaata ttgggaccag 240
 acataccatc ccaattgtat taactgtttg gatgataggt gtatccttca ttgtgcaaac 300
 tttaatgtgt tattttctac tgtgtttcca cctacaagct ttggaccact agtaagaaaa 360
 atattttag atggtgttcc tttgttgtt tcaactggat accat 405

<210> 120
 <211> 562
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<220>
 <221> misc_feature
 <222> (67)..(67)
 <223> n is a, c, g, or t

<400> 120
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 tgtattnaca atacattaga aagttacatg atgagcttac tggccacatg ttggacatgt 120
 attccgtaat gctaactaat gataacacct cacggtagtg ggaacctgag ttttatgagg 180
 ctatgtacac accacataca gtcttgacag ctgtagggtg ttgtgtattg tgcaattcac 240
 agacttcact tcgttgcggt gcctgtatta ggagaccatt cctatgttgc aagtgtgtgt 300
 atgaccatgt catttcaaca tcacacaaat tagtgttgtc tgtaaatccc tatgtttgca 360
 atgccccagg ttgtgatgtc actgatgtga cacaactgta tctaggaggt atgagctatt 420
 attgcaagtc acataagcct cccattagtt ttccattatg tgctaattgt cagggtttttg 480
 gttatacaa aaacacatgt gtaggcagtg acaatgtcac tgacttcaat gcgatagcaa 540
 catgtgattg gactaatgct gg 562

<210> 121

<211> 580
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 121
 gctatgtaca caccacatac agtcttgacag gctgtaggtg cttgtgtatt gtgcaattca 60
 cagacitcac ttcgttgagg tgccgtgtatt aggagaccat tcctatgttg caagtgcgtgc 120
 tatgaccatg tcattttcaac atcacacaaa ttagtggttg ctgttaatcc ctatgtttgc 180
 aatgccccag gttgtgatgt cactgatgtg acacaactgt atctaggagg tatgagctat 240
 tattgcaagt cacataagcc tcccattagt ttccattat gtgctaattg tcagggtttt 300
 ggtttatata aaaacacatg tgtaggcagt gacaatgtca ctgacttcaa tgcgatagca 360
 acatgtgatt ggactaatgc tggcgattac atacttgcca acacttgtag tgagagactc 420
 aagcttttcg cagcagaaac gctcaaagcc actgaggaaa catttaagct gtcatatggt 480
 attgccactg tacgcgaagt actctctgac agagaattgc atctttcatg ggagggttga 540
 aaacctagac caccattgaa cagaaactat gtctttactg 580

<210> 122
 <211> 610
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 122
 tgggtgatgct gttgtgtaca gaggtactac gacatacaag ttgaatgttg gtgattactt 60
 tgtgttgaca tctcacaactg taatgccact tagtgcacct actctagtgc cacaagagca 120
 ctatgtgaga attactggct tgtacccaac actcaacatc tcagatgagt ttcttagcaa 180
 tgttgcaaat tatcaaaagg tcggcatgca aaagtaactc aactccaag gaccacctgg 240
 tactggtaag agtcattttg ccatcggact tgctctctat taccatctg ctgcgatagt 300
 gtatacggca tgctctcatg cagctgttga tgccctatgt gaaaaggcat taaaatattt 360
 gcccatagat aaatgtagta gaatcatacc tgcgcgtgag cgcgtagagt gttttgataa 420
 attcaaagtg aattcaacac tagaacagta tgttttctgc actgtaaatt cattgccaga 480
 aacaactgct gacattgtag tctttgatga aatctctatg gctactaatt atgacttgag 540
 tgttgtcaat gctagacttc gtgcaaaaca ctacgtctat attggcgatc ctgctcaatt 600
 accagccct 610

<210> 123
 <211> 429
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 123

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ccaacactca acatctcaga tgagttttct agcaatgttg caaattatca aaaggtcggc      60
atgcaaaagt actctacact ccaaggacca cctgggtactg gtaagagtca ttttgccatc     120
ggacttgctc tctattacco atctgctcgc atagtgtata cggcatgctc tcatgcagct     180
gttgatgccc tatgtgaaaa ggcattaaaa tatttgccca tagataaatg tagtagaatc     240
atacctgcgc gtgcgcgcgt agagtgtttt gataaattca aagtgaattc aacactagaa     300
cagtatgttt tctgcactgt aaatgcattg ccagaaacaa ctgctgacat tgtagtcttt     360
gatgaaatct ctatggctac taattatgac ttgagtgttg tcaatgctag acttcgtgca     420
aaacactac                                         429

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<210> 124

<211> 486

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 124

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caatgtggct atcacaaggc caaaaattgg cattttgtgc ataatgtctg atagagatct      60
ttatgacaaa ctgcaattta caagtctaga aataccacgt cgcaatgtgg ctacattaca     120
agcagaaaat gtaactggac tttttaagga ctgtagtaag atcattactg gtcttcatcc     180
tacacaggca cctacacacc tcagcgttga tataaagttc aagactgaag gattatgtgt     240
tgacatacca ggcataccaa aggacatgac ctaccgtaga ctcatctcta tgatggggtt     300
caaaatgaat taccaagtca atggttaccc taatatgttt atcaccgcgc aagaagctat     360
tcgtcacgtt cgtgcgtgga ttggctttga tgtagagggc tgtcatgcaa ctagagatgc     420
tgtgggtact aacctacctc tcagctaggc attttctaca ggtgttaact tagtagctgt     480
accgac                                         486

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<210> 125

<211> 427

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 125

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aaaggacatg acctaccgta gactcatctc tatgatgggt ttcaaaatga attaccaagt      60
caatgggttac cctaatatgt ttatcaccgc cgaagaagct attcgtcacg ttcgtgcgtg     120
gattggcttt gatgtagagg gctgtcatgc aactagagat gctgtgggta ctaacctacc     180
tctccagcta ggattttcta cagggtgttaa cttagtagct gtaccgactg gttatgttga     240
cactgaaaat aacacagaat tcaccagagt taatgcaaaa cctccaccag gtgaccagtt     300
taaacatctt ataccactca tgtataaagg cttgccctgg aatgtagtgc gtattaagat     360
agtacaaatg ctcagtgata cactgaaagg attgtcagac agagtcgtgt tcgtcctttg     420

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ggcgcat

427

<210> 126

<211> 392

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 126

atggaaatgc acatgtggct agttgtgatg ctatcatgac tagatgttta gcagtccatg 60

agtgccttgt taagcgcggt gattggctctg ttgaataccc tattatagga gatgaactga 120

gggttaattc tgcttgcaga aaagtacaac acatgggtgt gaagtctgca ttgcttgctg 180

ataagtttcc agttcttcat gacattggaa atccaaaggc tatcaagtgt gtgcctcagg 240

ctgaagtaga atggaagttc tacgatgctc agccatgtag tgacaaagct taaaaaatag 300

aggaactctt ctattcttat gctacacatc acgataaatt cactgatggt gtttgcttgt 360

tttgggaattg taacgttgat cgttaccag cc 392

<210> 127

<211> 483

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 127

gcttcatcag atacttatgc ctgctggaat cattctgtgg gttttgacta tgtctataac 60

ccatttatga ttgatgttca gcagtggggc tttacgggta accttcagag taaccatgac 120

caacattgcc aggtacatgg aaatgcacat gtggctagtt gtgatgctat catgactaga 180

tgttttagcag tccatgagtg ctttggttaag cgcgttgatt ggtctgttga ataccctatt 240

ataggagatg aactgagggt taattctgct tgcagaaaag tacaacacat ggttgtgaag 300

tctgcattgc ttgctgataa gtttccagtt cttcatgaca ttggaaatcc aaaggctatc 360

aagtgtgtgc ctcaggctga agtagaatgg aagttctacg atgctcagcc atgtagtac 420

aaagcttaca aaatagagga actcttctat tottatgcta cacatcacga taaattcact 480

gat 483

<210> 128

<211> 326

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 128

tcaaagggac cagcacaagc tagcgtcaat ggagtcacat taattggaga atcagtaaaa 60

acacagttta actactttaa gaaagtagac ggcattattc aacagttgcc tgaaacctac 120

tttactcaga gcagagactt agaggatttt aagcccagat cacaaatgga aactgacttt 180

ctcgagctcg ctatggatga attcatacag cgatataagc tcgagggcta tgcottcgaa 240
 cacatcgttt atggagattt cagtcattga caacttggcg gtcttcattt aatgataggg 300
 ttagccaagc gctcacaaga ttcaact 326

<210> 129
 <211> 457
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 129
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 gtaaaaacac agtttaacta ctttaagaaa gtagacggca ttattcaaca gttgcctgaa 120
 acctacttta ctgagagcag agacttagag gatttttaagc ccagatcaca aatggaaact 180
 gactttctcg agctcgctat ggatgaattc atacagcgat ataagctcga gggctatgcc 240
 ttcgaacaca tcgtttatgg agatttcagt catggacaac ttggcgggtct tcattttaatg 300
 ataggcttag ccaagcgctc acaagattca ccacttaaact tagaggattt tatccctatg 360
 gacagcacag tgaaaaatta cttcataaca gatgcgcaaa caggttcctc aaaatgtgtg 420
 tgttctgtga ttgatctttt acttgatgac tttgtcgc 457

<210> 130
 <211> 493
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 130
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 catgagagtt attcactttg gtgctggctc tgataaagga gttgcaccag gtacagctgt 120
 gctcagacaa tggtttgcaa ctggcacact acttgctgat tcagatctta atgacttcgt 180
 ctccgacgca gattctactt taattggaga ctgtgcaaca gtacatcagg ctaataaatg 240
 ggaccttatt attagcgata tgtatgaccc taggaacaaa catgtgacaa aagagaatga 300
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 tggttctata gctgtaaaga taacagagca ttctttggaat gctgaccttt acaagcttat 420
 gggccatttc tcatggtgga cagcttttgt tacaatgta aatgcatcat catcggaagc 480
 atttttaatt ggg 493

<210> 131
 <211> 490
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 131
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 gctctgataa aggagttgca ccagggtacag ctgtgctcag acaatgggtg ccaactggca 120
 cactacttgt cgattcagat cttaatgact tcgtctccga cgcagattct actttaattg 180
 gagactgtgc aacagtacat acggctaata aatgggacct tattattagc gatatgtatg 240
 accctaggac caaacatgtg acaaaagaga atgactctaa agaagggttt ttcacttato 300
 tgtgtggatt tataaagcaa aaactagccc tgggtgggtc tatagctgta aagataacag 360
 agcattcttg gaatgotgac ctttacaagc ttatgggcca tttctcatgg tggacagctt 420
 ttgttacaaa tgtaaagca tcatcatcgg aagcattttt aattggggct aactatcttg 480
 gcaagccgaa 490

<210> 132
 <211> 550
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 132
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 tagagaaaac aacagagttg tggtttcaag tgatattctt gttaacaact aaacgaacat 120
 gtttattttc ttattatttc ttactctcac tagtggtagt gaccttgacc ggtgcaccac 180
 ttttgatgat gttcaagctc ctaattacac tcaacatact tcatctatga ggggggttta 240
 ctatcctgat gaaattttta gatcagacac tctttattta actcaggatt tatttcttcc 300
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 ggtttttggg tctaacatga acaacaagtc acagtcgggtg attattatta acaattctac 480
 taatgttggt atacgagcat gtaactttga attgtgtgac aacctttct ttgtgtttc 540
 taaaccata 550

<210> 133
 <211> 490
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 133
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 gctctgataa aggagttgca ccagggtacag ctgtgctcag acaatgggtg ccaactggca 120
 cactacttgt cgattcagat cttaatgact tcgtctccga cgcagattct actttaattg 180
 gagactgtgc aacagtacat acggctaata aatgggacct tattattagc gatatgtatg 240

accctaggac caaacatgtg acaaaagaga atgactctaa agaagggttt ttcacttatac 300
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 agcattcttg gaatgctgac ctttacaagc ttatgggccca tttctcatgg tggacagcgtt 420
 ttgttacaaa tgtaaatgca tcatcatcgg aagcattttt aattggggct aactatcttg 480
 gcaagccgaa 490

<210> 134
 <211> 550
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 134
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 gtttattttc ttattatttc ttactctcac tagtggtagt gacctgacc ggtgcaccac 180
 ttttgatgat gttcaagctc ctaattacac tcaacatact tcatctatga ggggggttta 240
 ctatcctgat gaaattttta gatcagacac tctttattta actcaggatt tatttcttcc 300
 attttattct aatgttacag ggtttcatac tattaatcat acgtttggca accctgtcat 360
 accttttaag gatggtatatt attttgctgc cacagagaaa tcaaagtgtg tccgtggttg 420
 ggtttttggt tctaccatga acaacaagtc acagtcgggtg attattatta acaattctac 480
 taatgttggt atacgagcat gtaactttga attgtgtgac aaccctttct ttgctgtttc 540
 taaaccata 550

<210> 135
 <211> 400
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 135
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 agagttgtgg tttcaagtga tattcttggt aacaactaaa cgaacatgtt tattttctta 120
 ttatttctta ctctcactag tggtagtgac cttgaccggt gcaccacttt tgatgatggt 180
 caagctccta attacactca acatacttca tctatgaggg gggtttacta tctgatgaa 240
 attttttagat cagacactct ttatttaact caggatttat ttcttcatt ttattctaata 300
 gttacagggt ttcatactat taatcatatc tttggcaacc ctgtcatacc ttttaaggat 360
 ggtatttatt ttgctgccac agagaaatca aatgttgtcc 400

<210> 136
 <211> 288

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 136

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tgatctttgc ttctccaatg tctatgcaga ttctttggta gtcaagggag atgatgtaag      60
acaaatagcg ccaggacaaa ctggtgttat tgctgattat aattataaat tgccagatga      120
tttcatgggt tgtgtccttg cttggaatac taggaacatt gatgctactt caactggtaa      180
ttataattat aaatataggt atcttagaca tggcaagctt aggccctttg agagagacat      240
atctaattgt cctttctcca cctgatggca aaccttgcac cccacctg      288

```

<210> 137

<211> 411

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 137

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ctttgagaga gacatatcta atgtgccttt ctcccctgat ggcaaacctt gcaccccacc      60
tgctcttaat tgttattggc cattaaatga ttatggtttt tacaccacta ctggcattgg      120
ctaccaacct tacagagttg tagtactttc ttttgaactt ttaaattgcac cggccacggg      180
ttgtggacca aaattatcca ctgaccttat taagaaccag tgtgtcaatt ttaatttttaa      240
tggaactcact ggtactgggtg tgtaactcc ttcttcaaag agatttcaac catttcaaca      300
aattttgccg tgatgtttct gatttcactg attccgttcg agatcctaaa acatctgaaa      360
tattagacat ttcacctgc gcttttgggg gtgtaagtgt aattacacct g      411

```

<210> 138

<211> 357

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 138

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tggaatatatt ttggtggttt taatttttca caaatattac ctgacctct aaagccaact      60
aagaggtctt ttattgagga ctgctcttt aataagggtga cactcgctga tgctggcttc      120
atgaagcaat atggcgaatg cctaggtgat attaatgcta gagatctcat ttgtgogcag      180
aagttcaatg gacttacagt gttgccacct ctgctcactg atgatatgat tgctgcctac      240
actgctgctc tagttagtgg tactgccact gctggatgga catttggtgc tggcgctgct      300
cttcaaatac cttttgctat gcaaatggca tataggttca atggcattgg agttact      357

```

<210> 139

<211> 434

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 139

caatatggcg aatgcctagg tgatattaat gctagagatc tcatttgtgc gcagaagttc 60
 aatggactta cagtgttgcc acctctgctc actgatgata tgattgctgc ctacactgct 120
 gctctagtta gtggtactgc cactgctgga tggacatttg gtgctggcgc tgctcttcaa 180
 ataccttttg ctatgcaaata ggcatatagg ttcaatggca ttggagttac ccaaaatggt 240
 ctctatgaga accaaaaaca aatcgccaac caatttaaca aggcgattag tcaaattcaa 300
 gaatcactta caacaacatc aactgcattg ggcaagctgc aagacgttgt taaccagaat 360
 gctcaagcat taaacacact tgtaaacaac cttagctcta attttgggtgc aatttcaagt 420
 gtgctaaatg atat 434

<210> 140
 <211> 557
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 140
 acagacaata catttgtctc aggaaattgt gatgtcgtta ttggcatcat taacaacaca 60
 gtttatgata ctctgcaacc tgagcttgac tcattcaaag aagagctgga caagtacttc 120
 aaaaatcata catcaccaga tgttgatctt ggcgacattt caggcattaa cgcttctgtc 180
 gtcaacattc aaaaagaaat tgaccgcctc aatgaggtcg ctaaaaattt aaatgaatca 240
 ctcatgagcc ttcaagaatt gggaaaatat gagcaatata ttaaatggcc ttggtatggt 300
 tggcteggct tcattgctgg actaattgcc atcgatcatg ttacaatctt gctttgttgc 360
 atgactagtt gttgcagttg cctcaaggtt gcatgctctt gtggttcttg ctgcaagttt 420
 gatgaggatg actctgagcc agttctcaag ggtgtcaaata tacattacac ataaacgaac 480
 ttatggattt gtttatgaga ttttttactc ttagatcaat tactgcacag ccagtaaaaa 540
 ttgacaatgc ttctcct 557

<210> 141
 <211> 530
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 141
 atgtttggct cggcttcatt gctggactaa ttgccatcgt catggttaca atcttgcttt 60
 gttgcatgac tagttgttgc agttgcctca aggggtgcatg ctcttggtgt tcttgcgtga 120
 agtttgatga ggatgactct gagccagttc tcaagggtgt caaattacat tacacataaa 180
 cgaacttatg gatttgttta tgagattttt tactcttaga tcaattactg cacagocagt 240
 aaaaattgac aatgcttctc ctgcaagtac tgttcatgct acagcaacga taccgctaca 300
 agcctcactc cctttcggat ggcttggtat tggcggttga tttcttgctg tttttcagag 360

cgctaccaaa ataattgcgc tcaataaaaag atggcagcta gccctttata agggcttcca 420
 gttcatttgc aatttactgc tgctatttgt taccatctat tcacatcttt tgcttgtcgc 480
 tgcaggtatg gaggcgcaat ttttgtacct ctatgccttg atatattttc 530

<210> 142
 <211> 320
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 142
 ttgctcgtac ccgctcaatg tggtcattca accagaaaac aaacattctt ctcaatgtgc 60
 ctctccgggg gacaattgtg accagaccgc tcatggaaag tgaacttgtc attggtgctg 120
 tgatcattcg tggtcacttg cgaatggccg gacactccct agggcgctgt gacattaagg 180
 acctgccaaa agagatcact gtggctacat cacgaacgct ttcttattac aaattaggag 240
 cgtcgcagcg ttaggcact gattcagggt ttgctgcata caaccgctac cgtattggaa 300
 actataaatt aaatacagac 320

<210> 143
 <211> 417
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 143
 cgaacttatg tactcattcg ttctcggaaga aacaggtagc ttaatagtta atagcgtact 60
 tctttttctt gctttcgtgg tattcttgcct agtcacacta gccatcctta ctgcgcttcg 120
 attgtgtgcg tactgctgca atattgttaa cgtgagttta gtaaaaccaa cggtttacgt 180
 ctactcgcgt gttaaaaaatc tgaactcttc tgaaggagtt cctgatcttc tggctctaaac 240
 gaactaacta ttattattat tctgtttgga actttaacat tgcttatcat ggcagacaac 300
 ggtactatta ccgttgagga gcttaaacaa ctcttggaac aatggaacct agtaataggt 360
 ttctatttcc tagcctggat tatgttacta caatttgcct attctaatacg gaacagg 417

<210> 144
 <211> 516
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 144
 cttgtcattg gtgctgtgat cattcgtggc cacttgcgaa tggccggaca ctccctaggg 60
 cgctgtgaca ttaaggacct gccaaaagag atcaactgtg ctacatcacg aacgctttct 120
 tattacaaat taggagcgtc gcagcgtgta ggcactgatt caggttttgc tgcatacaac 180
 cgctaccgta ttggaaaacta taaattaaat acagaccacg ccggtagcaa cgacaatatt 240

gctttgctag tacagtaagt gacaacagat gtttcatott gttgacttcc aggttacaat 300
 agcagagata ttgattatca ttatgaggac tttcaggatt gctatttgga atcttgacgt 360
 tataataagt tcaatagtga gacaattatt taagcctcta actaagaaga attattcgga 420
 gttgatgat gaagaacctt tggagttaga ttatccataa aacgaacatg aaaattattc 480
 tcttcctgac attgatttta ttacatott gcgagc 516

<210> 145
 <211> 310
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 145
 cgatgtttca tcttggtgac ttccaggtta caatagcaga gatattgatt atcattatga 60
 ggactttcag gattgctatt tggaatcttg acgttataat aagttcaata gtgagacaat 120
 tatttaagcc tctaactaag aagaattatt cggagttaga tgatgaagaa cctatggagt 180
 tagattatcc ataaaacgaa catgaaaatt attctcttcc tgacattgat tgtatttaca 240
 tcttgcgagc tatatcacta tcaggagtgt gttagaggta cgactgtact actaaaagaa 300
 ccttgcccat 310

<210> 146
 <211> 556
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 146
 agaaagacag aatgaatgag ctacttttaa ttgacttcta tttgtgcttt ttagcctttc 60
 tgctattcct tgtttttaata atgcttatta ttttttggtt ttactctgaa atccaggatc 120
 tagaagaacc ttgtacccaa gtctaaacga acatgaaact tctcattggt ttgacttgta 180
 tttctctatg cagttgcata tgcactgtag tacagcgctg tgcacttaat aaacctcatg 240
 tgcttgaaga tccttgtaag gtacaacact aggggtaata ctatagcac tgcttggctt 300
 tgtgctctag gaaaggtttt accttttcat agatggcaca ctatgggttca aacatgcaca 360
 cctaatgtta ctatcaactg tcaagatcca gctgggtggtg cgcttatagc taggtgttgg 420
 taccttcatg aagggtcacca aactgctgca tttagagacg tacttgttgt tttaaataaa 480
 cgaacaaatt aaaatgtctg ataatggacc ccaatcaaac caacgtagtg cccccgcac 540
 tacatttggt ggaccc 556

<210> 147
 <211> 110
 <212> DNA

<213> Severe acute respiratory syndrome virus

<400> 147

acgaacatga aaattattct cttcctgaca ttgattgtat ttacatcttg cgagctatat 60

cactatcagg agtgtgttag aggtacgact gtactactaa aagaaccttg 110

<210> 148

<211> 363

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 148

gcatttagag acgtacttgt tgttttaaat aaacgaacaa attaaaatgt ctgataatgg 60

acctcaatca agccaacgta gtgcccccg cattacatctt ggtggacca cagattcaac 120

tgacaataac cagaatggag gacgcaatgg ggcaaggcca aaacagcgcc gaccccaagg 180

tttaccat aatactgctt cttgggtcac agctctcact cagcatggca aggaggaact 240

tagattccct cgaggccagg gcgttcacat caacaccaat agtggtccag atgaccaaact 300

tggtactac cgaagagcta cccgacgagt tcgtggtggt gacggcaaaa tgaaagagct 360

cag 363

<210> 149

<211> 294

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 149

ctatcagctg cgtgcaagat cagtttcacc aaaacttttc atcagacaag aggaggttca 60

acaagagctc tactcgccac tttttctcat tgttgctgct ctagtatttt taatactttg 120

cttcaccatt aagagaaaga cagaatgaat gagctcactt taattgactt ctatttgtgc 180

tttttagcct ttctgctatt cttgtttta ataatgctta ttatattttg gttttcactc 240

gaaatccagg atctagaaaa accttgtacc aaaggctaaa cgaacatgaa actt 294

<210> 150

<211> 504

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 150

caaactgctg catttagaga cgtacttggt gtttaaataa acgaacaaat taaaatgtct 60

gataatggac cccaatcaaa ccaacgtagt gcccccgca ttacatttgg tggaccocaca 120

gattcaactg acaataacca gaatggagga cgcaatgggg caaggccaaa acagcgccga 180

ccccagggtt taccataata tactgctgtt tgggttcacag ctctcactca gcatggcaag 240

gaggaaacta gattccctcg aggccagggc gttccaatca acaccaatag tgggtccagat 300

gaccaaattg gctactaccg aagagctacc cgacgagttc gtggtggtga cggcaaaatg 360
 aaagagctca gccccagatg gtacttctat tacctaggaa ctggcccaga agcttcactt 420
 ccctacggcg ctaacaaaga aggcacgta tgggttgcaa ctgagggagc cttgaataca 480
 cccaagacc acattggcac ccgt 504

<210> 151
 <211> 474
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 151
 ctgcgcactt tttctcattg ttgctgctct agtattttta atactttgct tcaccattaa 60
 gagaaagaca gaatgaatga gctcacttta attgacttct atttgtgctt tttagccttt 120
 ctgctattcc ttgttttaaat aatgcttatt atatttttgggt tttcactcga aatccaggat 180
 ctagaagaac cttgtaccaa agtctaaacg aacatgaaac ttctcattgt tttgacttgt 240
 atttctctat gcagttgcat atgcactgta gtacagcgct gtgcatctaa taaacctcat 300
 gtgcttgaag atccttgtaa ggtacaacac taggggtaat acttatagca ctgcttggct 360
 ttgtgctcta ggaaaggttt taccttttca tagatggcac actatggttc aaacatgcac 420
 acctaattgtt actatcaact gtcaagatcc agctgggtgggt gcgcttatag ctag 474

<210> 152
 <211> 516
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 152
 cattaagaga aagacagaat gaatgagctc actttaattg acttctattt gtgctttttta 60
 gcctttctgc tattccttgt ttttaataatg cttattatat tttggttttc actcgaaatc 120
 caggatctag aagaaccttg taccaaagtc taaacgaaca tgaaacttct cattgttttg 180
 acttgtattt ctctatgcag ttgcatatgc actgtagtac agcgctgtgc atctaataaa 240
 cctcatgtgc ttgaagatcc ttgtaaggta caacactagg ggttaatactt atagcactgc 300
 ttggctttgt gctctaggaa aggttttacc ttttcataga tggcacacta tggttcaaac 360
 atgcacacct aatgttacta tcaactgtca agatccagct ggtggtgcgc ttatagctag 420
 gtgttggtac cttcatgaag gtcaccaaac tgctgcattt agagacgtac ttgttggttt 480
 aaataaacga acaaattaaa atgtctgata atggac 516

<210> 153
 <211> 451
 <212> DNA

<213> Severe acute respiratory syndrome virus

<400> 153

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ccaaggttta cccaataata ctgcgtcttg gttcacagct ctactcagc atggcaagga      60
ggaacttaga ttccctcgag gccagggcgt tccaatcaac accaatagtg gtccagatga      120
ccaaattggc tactaccgaa gagctacccg acgagttcgt ggtgggtgacg gcaaaatgaa      180
agagctcagc ccagatgggt acttctatta cctaggaact ggcccagaag cttcacttcc      240
ctacggcgct aacaaagaag gcatcgatat gggttgcaact gagggagcct tgaatacacc      300
caaagaccac attggcaccg gcaatcctaa taacaatgct gccaccgtgc tacaacttcc      360
tcaaggaaca acattgccaa aaggcttcta cgcagagggg agcagagggc gcagtcaagc      420
ctcttctcgc tctcatcac gtagtcgogg t                                451
```

<210> 154

<211> 495

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 154

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gatgaagctc agcctttgcc gcagagacaa aagaagcagc cactgtgac tcttcttcct      60
goggctgaca tggatgattt ctccagacaa cttcaaaatt ccatgagtgg agcttctgct      120
gattcaactc aggcataaac actcatgatg accacacaag gcagatgggc tatgtaaagc      180
ttttcgcaat tccgtttacg atacatagtc tactcttggt cagaatgaat tctcgtaact      240
aaacagcaca agtaggttta gttaacttta atctcacata gcaatcttta atcaatgtgt      300
aacattaggg aggacttgaa agagccacca ctttttcacg gaggccacgc ggagtacgat      360
cgagggtaca gtgaataatg ctagggagag ctgcctatat ggaagagccc taatgtgtaa      420
aattaatttt agtagtgcta tccccatgtg attttaatag cttcttagga gaatgacaaa      480
aaaaaaaaaa aaaaaa                                495
```

<210> 155

<211> 512

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 155

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acaaggccaa actgtcacta agaaatctgc tgctgaggca tctaaaaagc ctcgccaaaa      60
acgtactgcc aaaaaacagt acaacgtcac tcaagcattt gggagacgtg gtccagaaca      120
aacccaagga aatttcgggg accaagacct aatcagacaa ggaactgatt acaaacattg      180
gcgcgcaatt gcacaatttg ctccaagtgc ctctgcattc tttggaatgt cagcgattgg      240
catggaagtc acaccttcgg gaacatggct gacttatcat ggagccatta aattggatga      300
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caaagatcca caattcaaag acaacgtcat actgctgaac aagcacattg acgcatacaa 360
 aacattccca ccaacagagc ctaaaaagga caaaaagaaa aagactgatg aagctcagcc 420
 tttgccgcag agacaaaaga agcagcccac tgtgactcct ctccctgcgg ctgatatgga 480
 tgatttctcc agacaacttc aaaattccat ga 512

<210> 156
 <211> 442
 <212> DNA
 <213> Severe acute respiratory syndrome virus

<400> 156
 tgtgactcct ctccctgcgg ctgatatgga tgtttctcca gacaacttca aaattccatg 60
 agtggagcct ctgctgattc aactcagga taaacactca tgatgaccac acaaggcaga 120
 tgggctatgt aaacgttttc gcaattccgt ttacgataca tagtctactc ttgtgcagaa 180
 tgaattctcg taactaaaca gcacaagtag gtttagttaa ctttaatctc acatagcaat 240
 ctttaatcaa tgtgtaacat tagggaggac ttgaaagagc caccacattt tcatcgaggc 300
 cagcgggagt acgatcgagg gtacagtga taaatgctagg gagagctgcc tatatggaag 360
 agccctaatt tgtaaaatta attttagtag tgctatcccc atgtgatttt aatagcttct 420
 taggagaatg acaaaaaaaaa aa 442

<210> 157
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 157
 atgaattacc aagtcaatgg ttac 24

<210> 158
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 158
 gaagctattc gtcacgttcg 20

<210> 159
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Primer

<400> 159
ctgtagaaaa tcctagctgg ag 22

<210> 160
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 160
cataaccagt cggtacagct a 21

<210> 161
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 161
ttatcacccg cgaagaagct 20

<210> 162
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 162
ctctagttgc atgacagccc tc 22

<210> 163
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 163
tcgtgcgtgg attggctttg atgt 24

<210> 164
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 164

gggttgggac taccctaagt gtga

24

<210> 165

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 165

taacacacaa acaccatcat ca

22

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 166

gggttgggact atcctaagtq tga

23

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 167

ccatcatcag atagaatcat cata

24

<210> 168

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 168

cctctcttgt tcttgctcgc a

21

<210> 169

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 169
tatagtgāgc cgccacacat g 21

<210> 170
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<400> 170
taacacacaa cncatcatc a 21

<210> 171
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 171
ctaacatgct taggataatg g 21

<210> 172
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 172
gcctctcttg ttcttgctcg c 21

<210> 173
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 173
caggtaagcg taaaactcat c 21

<210> 174
<211> 17

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 174
tacacacctc agcggtg

17

<210> 175
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 175
cacgaacgtg acgaat

16

<210> 176
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 176
gccgagctc tgcagaattc

20

<210> 177
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 177
caggaaacag ctatgacttg catcaccact agttgtgcc a ccaggtt

47

<210> 178
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 178
tgtaaaacga cggccagttg atgggatggg actatcctaa gtgtga

46

<210> 179
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 179

gcataggcag tagttgcatc

20

<210> 180

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> ATP Binding Domain

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = A or G

<220>

<221> misc_feature

<222> (2)..(5)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa = S or T

<400> 180

Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa

1

5

<210> 181

<211> 23

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 181

Trp Tyr Val Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met

1

5

10

15

Val Thr Ile Leu Leu Cys Cys

20

<210> 182

<211> 16

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 182

Met Asp Leu Phe Met Arg Phe Phe Thr Leu Arg Ser Ile Thr Ala Gln
 1 5 10 15

<210> 183
 <211> 150
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 183

Met Arg Cys Trp Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu
 1 5 10 15

Tyr Asp Ala Asn Tyr Phe Val Cys Trp His Thr His Asn Tyr Asp Tyr
 20 25 30

Cys Ile Pro Tyr Asn Ser Val Thr Asp Thr Ile Val Val Thr Glu Gly
 35 40 45

Asp Gly Ile Ser Thr Pro Lys Leu Lys Glu Asp Tyr Gln Ile Gly Gly
 50 55 60

Tyr Ser Glu Asp Arg His Ser Gly Val Lys Asp Tyr Val Val Val His
 65 70 75 80

Gly Tyr Phe Thr Glu Val Tyr Tyr Gln Leu Glu Ser Thr Gln Ile Thr
 85 90 95

Thr Asp Thr Gly Ile Glu Asn Ala Thr Phe Phe Ile Phe Asn Lys Leu
 100 105 110

Val Lys Asp Pro Pro Asn Val Gln Ile His Thr Ile Asp Gly Ser Ser
 115 120 125

Gly Val Ala Asn Pro Ala Met Asp Pro Ile Tyr Asp Glu Pro Thr Thr
 130 135 140

Thr Thr Ser Val Pro Leu
 145 150

<210> 184
 <211> 20
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 184

Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
 1 5 10 15

Val Tyr His Ile
20

<210> 185
<211> 42
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 185

Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn Val Ser
1 5 10 15

Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn Leu Asn
20 25 30

Ser Ser Glu Gly Val Pro Asp Leu Leu Val
35 40

<210> 186
<211> 39
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 186

Met Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu
1 5 10 15

Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
20 25 30

Leu Leu Gln Phe Ala Tyr Ser
35

<210> 187
<211> 100
<212> PRT
<213> Severe acute respiratory syndrome virus

<400> 187

Pro Leu Arg Gly Thr Ile Val Thr Arg Pro Leu Met Glu Ser Glu Leu
1 5 10 15

Val Ile Gly Ala Val Ile Ile Arg Gly His Leu Arg Met Ala Gly His
20 25 30

Ser Leu Gly Arg Cys Asp Ile Lys Asp Leu Pro Lys Glu Ile Thr Val
35 40 45

Ala Thr Ser Arg Thr Leu Ser Tyr Tyr Lys Leu Gly Ala Ser Gln Arg
 50 55 60

Val Gly Thr Asp Ser Gly Phe Ala Ala Tyr Asn Arg Tyr Arg Ile Gly
 65 70 75 80

Asn Tyr Lys Leu Asn Thr Asp His Ala Gly Ser Asn Asp Asn Ile Ala
 85 90 95

Leu Leu Val Gln
 100

<210> 188
 <211> 23
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 188

Phe Tyr Leu Cys Phe Leu Ala Phe Leu Leu Phe Leu Val Leu Ile Met
 1 5 10 15

Leu Ile Ile Phe Trp Phe Ser
 20

<210> 189
 <211> 19
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 189

Leu Leu Ile Val Leu Thr Cys Ile Ser Leu Cys Ser Cys Ile Cys Thr
 1 5 10 15

Val Val Gln

<210> 190
 <211> 24
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 190

Ile Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His Val Leu
 1 5 10 15

Glu Asp Pro Cys Lys Val Gln His
 20

<210> 191
 <211> 22
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 191

Cys Ile Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His Val
 1 5 10 15

Leu Glu Asp Pro Cys Lys
 20

<210> 192
 <211> 22
 <212> PRT
 <213> Severe acute respiratory syndrome virus

<400> 192

Val Val Ala Val Ile Gln Glu Ile Gln Leu Leu Ala Ala Val Gly Glu
 1 5 10 15

Ile Leu Leu Leu Glu Trp
 20

<210> 193
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 193
 aattcgcggc cgcgtcgac

19

<210> 194
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 194
 gtcgacgcgg ccgcg

15

<210> 195
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 195

aattcgcggc cgcgtcgac

19

<210> 196

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 196

ggcctcttcg ctattacgc

19

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 197

tgcaggtcga ctctagagga t

21

<210> 198

<211> 410

<212> PRT

<213> Avian infectious bronchitis virus

<400> 198

Met Ala Ser Gly Lys Ala Ala Gly Lys Thr Asp Ala Pro Ala Pro Val
1 5 10 15

Ile Lys Leu Gly Gly Pro Lys Pro Pro Lys Val Gly Ser Ser Gly Asn
20 25 30

Ala Ser Trp Phe Gln Ala Ile Lys Ala Lys Lys Leu Asn Thr Pro Pro
35 40 45

Pro Lys Phe Glu Gly Ser Gly Val Pro Asp Asn Glu Asn Ile Lys Pro
50 55 60

Ser Gln Gln His Gly Tyr Trp Arg Arg Gln Ala Arg Phe Lys Pro Gly
65 70 75 80

Lys Gly Gly Arg Lys Pro Val Pro Asp Ala Trp Tyr Phe Tyr Tyr Thr
85 90 95

Gly Thr Gly Pro Ala Ala Asp Leu Asn Trp Gly Asp Thr Gln Asp Gly
 100 105 110

Ile Val Trp Val Ala Ala Lys Gly Ala Asp Thr Lys Ser Arg Ser Asn
 115 120 125

Gln Gly Thr Arg Asp Pro Asp Lys Phe Asp Gln Tyr Pro Leu Arg Phe
 130 135 140

Ser Asp Gly Gly Pro Asp Gly Asn Phe Arg Trp Asp Phe Ile Pro Leu
 145 150 155 160

Lys Asn Arg Gly Arg Ser Gly Arg Ser Thr Ala Ala Ser Ser Ala Ala
 165 170 175

Ala Ser Arg Ala Pro Ser Arg Glu Gly Ser Arg Gly Arg Arg Ser Asp
 180 185 190

Ser Gly Asp Asp Leu Ile Ala Arg Ala Ala Lys Ile Ile Gln Asp Gln
 195 200 205

Gln Lys Lys Gly Ser Arg Ile Thr Lys Ala Lys Ala Asp Glu Met Ala
 210 215 220

His Arg Arg Tyr Cys Lys Arg Thr Ile Pro Pro Asn Tyr Arg Val Asp
 225 230 235 240

Gln Val Phe Gly Pro Arg Thr Lys Gly Lys Glu Gly Asn Phe Gly Asp
 245 250 255

Asp Lys Met Asn Glu Glu Gly Ile Lys Asp Gly Arg Val Thr Ala Met
 260 265 270

Leu Asn Leu Val Pro Ser Ser His Ala Cys Leu Phe Gly Ser Arg Val
 275 280 285

Thr Pro Lys Leu Gln Leu Asp Gly Leu His Leu Arg Phe Glu Phe Thr
 290 295 300

Thr Val Val Pro Cys Asp Asp Pro Gln Phe Asp Asn Tyr Val Lys Ile
 305 310 315 320

Cys Asp Gln Cys Val Asp Gly Val Gly Thr Arg Pro Lys Asp Asp Glu
 325 330 335

Pro Lys Pro Lys Ser Arg Ser Ser Ser Arg Pro Ala Thr Arg Gly Asn

cgatgtttca ttttgttgac ttccagggtta caatagcaga gatattgatt atcattatga 60
ggacttttcag gattgctatt tggaatcttg acgtttataat aagttcaata gtgagacaat 120
tattttaagcc tctaactaag aagaattatt cggagttaga tgatgaagaa cctatqqaqt 180

tagattatcc ataaaacgaa catgaaaatt attctcttcc tgacattgat tgtatttaca 240
 tcttgcgagc tatatcacta tcaggagtgt gtttagaggta cgactgtact actaaaagaa 300
 ccttgcccat 310

<210> 202

<211> 556

<212> DNA

<213> Severe acute respiratory syndrome virus

<400> 202

agaaagacag aatgaatgag ctcaacttta ttgacttcta tttgtgcttt ttagcctttc 60
 tgctattcct tgttttaata atgcttatta ttttttggtt ttcactcgaa atccaggatc 120
 tagaagaacc ttgtaccaa gtctaaacga acatgaaact tctcattggt ttgacttgta 180
 tttctctatg cagttgcata tgcaactgtag tacagcgctg tgcactctaat aaacctcatg 240
 tgcttgaaga tccttgtaag gtacaacact aggggtaata cttatagcac tgcttggctt 300
 tgtgctctag gaaagggttt accttttcat agatggcaca ctatgggttca aacatgcaca 360
 cctaattgta ctatcaactg tcaagatcca gctgggtggtg cgcttatagc taggtgttgg 420
 taccttcatg aaggtcacca aactgctgca tttagagacg tacttggttg tttaaataaa 480
 cgaacaaatt aaaatgtctg ataatggacc ccaatcaaac caacgtagtg cccccgcat 540
 tacaatttgggt ggaccc 556

<210> 203

<211> 1255

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 203

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
 1 5 10 15

Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
 20 25 30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
 35 40 45

Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
 50 55 60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
 65 70 75 80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
 85 90 95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
 100 105 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
 115 120 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
 130 135 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
 145 150 155 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
 165 170 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
 180 185 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
 195 200 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
 210 215 220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
 225 230 235 240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
 245 250 255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
 260 265 270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
 275 280 285

Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
 290 295 300

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
 305 310 315 320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser

	325		330		335
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr	340		345		350
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly	355		360		365
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala	370		375		380
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly	385		390		395
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe		405		410	415
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser	420		425		430
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu	435		440		445
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly	450		455		460
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp	465		470		475
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val		485		490	495
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly	500		505		510
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn	515		520		525
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg	530		535		540
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp	545		550		555
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys	565		570		575

Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620

Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690 695 700

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705 710 715 720

Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
725 730 735

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
740 745 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
755 760 765

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770 775 780

Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785 790 795 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
805 810 815

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
 820 825 830
 Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
 835 840 845
 Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
 850 855 860
 Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
 865 870 875 880
 Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
 885 890 895
 Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
 900 905 910
 Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
 915 920 925
 Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
 930 935 940
 Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
 945 950 955 960
 Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
 965 970 975
 Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
 980 985 990
 Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
 995 1000 1005
 Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
 1010 1015 1020
 Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
 1025 1030 1035
 Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
 1040 1045 1050

Glu	Arg	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Glu	Gly	Lys
1055						1060					1065			
Ala	Tyr	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Phe	Asn	Gly	Thr	Ser
1070						1075					1080			
Trp	Phe	Ile	Thr	Gln	Arg	Asn	Phe	Phe	Ser	Pro	Gln	Ile	Ile	Thr
1085						1090					1095			
Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	Ile	Gly
1100						1105					1110			
Ile	Ile	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	Leu	Asp
1115						1120					1125			
Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His	Thr	Ser
1130						1135					1140			
Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala	Ser	Val
1145						1150					1155			
Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val	Ala	Lys
1160						1165					1170			
Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly	Lys	Tyr
1175						1180					1185			
Glu	Gln	Tyr	Ile	Lys	Trp	Pro	Trp	Tyr	Val	Trp	Leu	Gly	Phe	Ile
1190						1195					1200			
Ala	Gly	Leu	Ile	Ala	Ile	Val	Met	Val	Thr	Ile	Leu	Leu	Cys	Cys
1205						1210					1215			
Met	Thr	Ser	Cys	Cys	Ser	Cys	Leu	Lys	Gly	Ala	Cys	Ser	Cys	Gly
1220						1225					1230			
Ser	Cys	Cys	Lys	Phe	Asp	Glu	Asp	Asp	Ser	Glu	Pro	Val	Leu	Lys
1235						1240					1245			
Gly	Val	Lys	Leu	His	Tyr	Thr								
1250						1255								

<210> 204

<211> 422

<212> PRT

<213> Severe acute respiratory syndrome virus

<400> 204

Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
 1 5 10 15

Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
 20 25 30

Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
 35 40 45

Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
 50 55 60

Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
 65 70 75 80

Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
 85 90 95

Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
 100 105 110

Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
 115 120 125

Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
 130 135 140

Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
 145 150 155 160

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
 165 170 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
 180 185 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
 195 200 205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
 210 215 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
 225 230 235 240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
245 250 255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
260 265 270

Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
275 280 285

Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
290 295 300

Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg
305 310 315 320

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
325 330 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
340 345 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
355 360 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
370 375 380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
385 390 395 400

Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
405 410 415

Ala Asp Ser Thr Gln Ala
420

<210> 205

<211> 221

<212> PRT

<213> Sars associated coronavirus

<400> 205

Met Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu
1 5 10 15

Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met

20 25 30
 Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
 35 40 45
 Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
 50 55 60
 Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
 65 70 75 80
 Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
 85 90 95
 Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
 100 105 110
 Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
 115 120 125
 Thr Arg Pro Leu Met Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile
 130 135 140
 Arg Gly His Leu Arg Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile
 145 150 155 160
 Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
 165 170 175
 Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
 180 185 190
 Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
 195 200 205
 His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val Gln
 210 215 220
 <210> 206
 <211> 76
 <212> PRT
 <213> Severe acute respiratory syndrome virus
 <400> 206
 Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
 1 5 10 15

Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
20 25 30

Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
35 40 45

Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
50 55 60

Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
65 70 75